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Goddard, Audrey  
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Kljavin, Ivar J.  
Kuo, Sophia S.  
Napier, Mary A.  
Pan, James;  
Paoni, Nicholas F.  
Roy, Margaret Ann  
Shelton, David L.  
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Tumas, Daniel  
Williams, P. Mickey  
Wood, William I.

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                   110                  115                  120  
  
 Asp Glu Ser Val Gly Ser Lys Thr Arg Arg Ala Phe Leu Tyr Leu  
                   125                  130                  135  
  
 Ala Ala Phe Pro Phe Met Asp Ala Met Ala Trp Thr His Ala Gly  
                   140                  145                  150  
  
 Ile Leu Leu Lys His Lys Tyr Ser Phe Leu Val Gly Cys Ala Ser  
                   155                  160                  165  
  
 Ile Ser Asp Val Ile Ala Gln Val Val Phe Val Ala Ile Leu Leu  
                   170                  175                  180  
  
 His Ser His Leu Glu Cys Arg Glu Pro Leu Leu Ile Pro Ile Leu  
                   185                  190                  195  
  
 Ser Leu Tyr Met Gly Ala Leu Val Arg Cys Thr Thr Leu Cys Leu  
                   200                  205                  210

Gly Tyr Tyr Lys	Asn Ile His Asp Ile	Ile Pro Asp Arg Ser	Gly
215		220	225
Pro Glu Leu Gly	Gly Asp Ala Thr Ile	Arg Lys Met Leu Ser	Phe
230		235	240
Trp Trp Pro Leu	Ala Leu Ile Leu Ala	Thr Gln Arg Ile Ser	Arg
245		250	255
Pro Ile Val Asn	Leu Phe Val Ser Arg	Asp Leu Gly Gly Ser	Ser
260		265	270
Ala Ala Thr Glu	Ala Val Ala Ile Leu	Thr Ala Thr Tyr Pro	Val
275		280	285
Gly His Met Pro	Tyr Gly Trp Leu Thr	Glu Ile Arg Ala Val	Tyr
290		295	300
Pro Ala Phe Asp	Lys Asn Asn Pro Ser	Asn Lys Leu Val Ser	Thr
305		310	315
Ser Asn Thr Val	Thr Ala Ala His Ile	Lys Lys Phe Thr Phe	Val
320		325	330
Cys Met Ala Leu	Ser Leu Thr Leu Cys	Phe Val Met Phe Trp	Thr
335		340	345
Pro Asn Val Ser	Glu Lys Ile Leu Ile	Asp Ile Ile Gly Val	Asp
350		355	360
Phe Ala Phe Ala	Glu Leu Cys Val Val	Pro Leu Arg Ile Phe	Ser
365		370	375
Phe Phe Pro Val	Pro Val Thr Val Arg	Ala His Leu Thr Gly	Trp
380		385	390
Leu Met Thr Leu	Lys Lys Thr Phe Val	Leu Ala Pro Ser Ser	Val
395		400	405
Leu Arg Ile Ile	Val Leu Ile Ala Ser	Leu Val Val Leu Pro	Tyr
410		415	420
Leu Gly Val His	Gly Ala Thr Leu Gly	Val Gly Ser Leu Leu	Ala
425		430	435
Gly Phe Val Gly	Glu Ser Thr Met Val	Ala Ile Ala Ala Cys	Tyr
440		445	450
Val Tyr Arg Lys	Gln Lys Lys Lys Met	Glu Asn Glu Ser Ala	Thr
455		460	465
Glu Gly Glu Asp	Ser Ala Met Thr Asp	Met Pro Pro Thr Glu	Glu
470		475	480
Val Thr Asp Ile	Val Glu Met Arg Glu	Glu Asn Glu	
485		490	

<210> 8  
<211> 535  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 33, 66, 96, 387  
<223> unknown base

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cggcctattg tcaacctctt tgtttcccg gaccttggtg gcagttctgc 150  
agccacagag gcagtggcga ttttgacagc cacataccct gtgggtcaca 200  
tgccatacgg ctggttgacg gaaatccgtg ctgtgtatcc tgctttcgac 250  
aagaataacc ccagcaacaa actggtgagc acgagcaaca cagtcacggc 300  
ggccacatc aagaagttca ccttcgtctg catggctctg tcactcacgc 350  
tctgtttcgt gatgttttgg acacccaacg tgtctgngaa aatcttgata 400  
gacatcatcg gagtggactt tgcccttgca gaactctgtg ttgttccttt 450  
gcggatcttc tccttcttcc cagttccagt cacagtgagg gcgcatctca 500  
ccgggtggct gatgacactg aagaaaacct tcgtc 535

<210> 9  
<211> 434  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 32, 54, 80, 111, 117, 122, 139, 193, 205, 221, 226, 228, 273,  
293, 296, 305, 336, 358, 361  
<223> unknown base

<400> 9  
tgacggaatc ccgggctggg tatectggtt tngacaagat aaacccccag 50  
caanaaattg gggagcaggg caaaacagtn acgggcagcc cacatcaaga 100  
agttcacctt ngtttgnatg gntctgtcaa ctcacgctnt gtttcgtgat 150  
gttttgagca cccaaagtgt ttgagaaaat tttgatagac atnatcggag 200  
tggantttgc ctttgacagaa ntttgnngtg ttcctttgcg gattttctcc 250  
tttttcccag ttccagtcac agngagggcg catctcaccg ggnggntgat 300

gacantgaag aaaacctttg tccttgcccc cagctntttg gtgcggatca 350  
ttgtcctnat ngccagcctt gtggtcctac cctacctggg ggtgcacggt 400  
gcgaccctgg gcgtgggttc cctcctggcg ggca 434

<210> 10  
<211> 154  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 33, 49, 68, 83, 90, 98, 119  
<223> unknown base

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tattcccgat tccggtcacg gggagggcgc atntcacgg gtggctgang 50  
acactgaaga aaaccttngt ccttgcccc agntttgtgn tgcggatnat 100  
cgtcctcatc gccagcctng tggctctacc ctacctgggg gtgcacggtg 150  
agac 154

<210> 11  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 11  
ctgatccggt tcttggtgcc cctg 24

<210> 12  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 12  
gctctgtcac tcacgctc 18

<210> 13  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 13  
tcattcttcc cctctccc 18

<210> 14  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 14  
ccttccgccca cggagtgc 18

<210> 15  
<211> 24  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 15  
ggcaaagtcc actccgatga tgct 24

<210> 16  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 16  
gcctgctgtg gtcacaggtc tccg 24

<210> 17  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 17  
tcggggagca ggccttgaac cggggcattg ctgctgtcaa ggagg 45

<210> 18  
<211> 1901  
<212> DNA  
<213> Homo sapiens

<400> 18  
gccccgcgcc cggcgccggg cgcccgaagc cgggagccac cgccatgggg 50  
gcctgcctgg gagcctgctc cctgctcagc tgcgcgtcct gcctctgcgg 100  
ctctgcccc tgcattcctg gcagctgctg ccccgccagc cgcaactcca 150



ccgtgagccg cctcatcttc acgttcttcc tcttctctggg ggtgctggtg 200  
tccatcatta tgctgagccc gggcgtggag agtcagctct acaagctgcc 250  
ctgggtgtgt gaggaggggg ccgggatccc caccgtcctg cagggccaca 300  
tcgactgtgg ctccctgctt ggctaccgcg ctgtctaccg catgtgcttc 350  
gccacggcgg ccttcttctt cttctttttt accctgctca tgetctgcgt 400  
gagcagcagc cgggaccccc gggctgccat ccagaatggg ttttggttct 450  
ttaagttcct gatcctggtg ggcctcaccg tgggtgcctt ctacatccct 500  
gacggctcct tcaccaacat ctggttctac ttcggcgtcg tgggctcctt 550  
cctcttcac ctcattccagc tgggtgctgct catcgacttt gcgcactcct 600  
ggaaccagcg gtggctgggc aaggccgagg agtgcgattc ccgtgcctgg 650  
tacgcaggcc tcttcttctt cactctcttc ttctacttgc tgtcgatcgc 700  
ggcgtggcg ctgatgttca tgtactacac tgagcccagc ggctgccacg 750  
agggcaaggt cttcatcagc ctcaacctca cttctgtgt ctgctgttcc 800  
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gctgcaggcc tcggatcatca ccctctacac catgtttgtc acctggtcag 900  
ccctatccag tatccctgaa cagaaatgca acccccattt gccaaccag 950  
ctgggcaacg agacagttgt ggcaggcccc gagggctatg agaccagtg 1000  
gtgggatgcc ccgagcattg tgggcctcat catcttcttc ctgtgcaccc 1050  
tcttcatcag tctgcgtccc tcagaccacc ggcaggtgaa cagcctgatg 1100  
cagaccgagg agtggccacc tatgctagac gccacacagc agcagcagca 1150  
gcaggtggca gcctgtgagg gccgggcctt tgacaacgag caggacggcg 1200  
tcacctacag ctactccttc ttccacttct gcctggtgct ggctcactg 1250  
cacgtcatga tgacgctcac caactggtac aagcccgggtg agaccggaa 1300  
gatgatcagc acgtggaccg ccgtgtgggt gaagatctgt gccagctggg 1350  
cagggtgct cctctacctg tggaccctgg tagccccact cctcctgcgc 1400  
aaccgcgact tcagctgagg cagcctcaca gcctgccatc tgggtgcctcc 1450  
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caccaatcag ccaggctgag cccccacccc tgccccagct ccaggacctg 1550  
cccctgagcc gggccttcta gtcgtagtgc cttcagggtc cgaggagcat 1600

caggctcctg cagagcccca tccccccgcc acaccacac ggtggagctg 1650  
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 agggctccct tgtcctcagg ctccacggga gcggggctgc tggagagagc 1750  
 ggggaactcc caccacagtg gggcatccgg cactgaagcc ctggtgttcc 1800  
 tggtcacgtc cccagggga ccctgcccc ttctggact tcgtgcctta 1850  
 ctgagtctct aagacttttt ctaataaaca agccagtgcg tgtaaaaaaa 1900  
 a 1901

<210> 19

<211> 457

<212> PRT

<213> Homo sapiens

<400> 19

Met	Gly	Ala	Cys	Leu	Gly	Ala	Cys	Ser	Leu	Leu	Ser	Cys	Ala	Ser	1	5	10	15
Cys	Leu	Cys	Gly	Ser	Ala	Pro	Cys	Ile	Leu	Cys	Ser	Cys	Cys	Pro	20	25	30	
Ala	Ser	Arg	Asn	Ser	Thr	Val	Ser	Arg	Leu	Ile	Phe	Thr	Phe	Phe	35	40	45	
Leu	Phe	Leu	Gly	Val	Leu	Val	Ser	Ile	Ile	Met	Leu	Ser	Pro	Gly	50	55	60	
Val	Glu	Ser	Gln	Leu	Tyr	Lys	Leu	Pro	Trp	Val	Cys	Glu	Glu	Gly	65	70	75	
Ala	Gly	Ile	Pro	Thr	Val	Leu	Gln	Gly	His	Ile	Asp	Cys	Gly	Ser	80	85	90	
Leu	Leu	Gly	Tyr	Arg	Ala	Val	Tyr	Arg	Met	Cys	Phe	Ala	Thr	Ala	95	100	105	
Ala	Phe	Phe	Phe	Phe	Phe	Phe	Thr	Leu	Leu	Met	Leu	Cys	Val	Ser	110	115	120	
Ser	Ser	Arg	Asp	Pro	Arg	Ala	Ala	Ile	Gln	Asn	Gly	Phe	Trp	Phe	125	130	135	
Phe	Lys	Phe	Leu	Ile	Leu	Val	Gly	Leu	Thr	Val	Gly	Ala	Phe	Tyr	140	145	150	
Ile	Pro	Asp	Gly	Ser	Phe	Thr	Asn	Ile	Trp	Phe	Tyr	Phe	Gly	Val	155	160	165	
Val	Gly	Ser	Phe	Leu	Phe	Ile	Leu	Ile	Gln	Leu	Val	Leu	Leu	Ile	170	175	180	

Asp	Phe	Ala	His	Ser 185	Trp	Asn	Gln	Arg	Trp 190	Leu	Gly	Lys	Ala	Glu 195
Glu	Cys	Asp	Ser	Arg 200	Ala	Trp	Tyr	Ala	Gly 205	Leu	Phe	Phe	Phe	Thr 210
Leu	Leu	Phe	Tyr	Leu 215	Leu	Ser	Ile	Ala	Ala 220	Val	Ala	Leu	Met	Phe 225
Met	Tyr	Tyr	Thr	Glu 230	Pro	Ser	Gly	Cys	His 235	Glu	Gly	Lys	Val	Phe 240
Ile	Ser	Leu	Asn	Leu 245	Thr	Phe	Cys	Val	Cys 250	Val	Ser	Ile	Ala	Ala 255
Val	Leu	Pro	Lys	Val 260	Gln	Asp	Ala	Gln	Pro 265	Asn	Ser	Gly	Leu	Leu 270
Gln	Ala	Ser	Val	Ile 275	Thr	Leu	Tyr	Thr	Met 280	Phe	Val	Thr	Trp	Ser 285
Ala	Leu	Ser	Ser	Ile 290	Pro	Glu	Gln	Lys	Cys 295	Asn	Pro	His	Leu	Pro 300
Thr	Gln	Leu	Gly	Asn 305	Glu	Thr	Val	Val	Ala 310	Gly	Pro	Glu	Gly	Tyr 315
Glu	Thr	Gln	Trp	Trp 320	Asp	Ala	Pro	Ser	Ile 325	Val	Gly	Leu	Ile	Ile 330
Phe	Leu	Leu	Cys	Thr 335	Leu	Phe	Ile	Ser	Leu 340	Arg	Ser	Ser	Asp	His 345
Arg	Gln	Val	Asn	Ser 350	Leu	Met	Gln	Thr	Glu 355	Glu	Cys	Pro	Pro	Met 360
Leu	Asp	Ala	Thr	Gln 365	Gln	Gln	Gln	Gln	Gln 370	Val	Ala	Ala	Cys	Glu 375
Gly	Arg	Ala	Phe	Asp 380	Asn	Glu	Gln	Asp	Gly 385	Val	Thr	Tyr	Ser	Tyr 390
Ser	Phe	Phe	His	Phe 395	Cys	Leu	Val	Leu	Ala 400	Ser	Leu	His	Val	Met 405
Met	Thr	Leu	Thr	Asn 410	Trp	Tyr	Lys	Pro	Gly 415	Glu	Thr	Arg	Lys	Met 420
Ile	Ser	Thr	Trp	Thr 425	Ala	Val	Trp	Val	Lys 430	Ile	Cys	Ala	Ser	Trp 435
Ala	Gly	Leu	Leu	Leu 440	Tyr	Leu	Trp	Thr	Leu 445	Val	Ala	Pro	Leu	Leu 450
Leu	Arg	Asn	Arg	Asp 455	Phe	Ser								

<210> 20  
<211> 24  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 20  
gccgcctcat cttcacgttc ttcc 24  
  
<210> 21  
<211> 20  
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<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 21  
tcatccagct ggtgctgctc 20  
  
<210> 22  
<211> 20  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 22  
cttcttcac ttctgcctgg 20  
  
<210> 23  
<211> 18  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 23  
cctgggcaaa aatgcaac 18  
  
<210> 24  
<211> 24  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 24  
caggaatgta gaaggacccc acgg 24  
  
<210> 25  
<211> 24

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 25  
tggcacagat cttcacccac acgg 24

<210> 26  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 26  
tgtccatcat tatgctgagc ccgggctgg agagtcagct ctacaagctg 50

<210> 27  
<211> 1351  
<212> DNA  
<213> Homo sapiens

<400> 27  
gagcgaggcc ggggactgaa ggtgtgggtg tcgagccctc tggcagaggg 50  
ttaacctggg tcaaatgcac ggattctcac ctctacagt tacgctctcc 100  
cgcggcacgt ccgcgaggac ttgaagtcct gagcgctcaa gtttgtccgt 150  
aggtcgagag aaggccatgg aggtgccgcc accggcaccg cggagctttc 200  
tctgtagagc attgtgccta tttccccgag tctttgctgc cgaagctgtg 250  
actgccgatt cggaagtcct tgaggagcgt cagaagcggc ttccctacgt 300  
cccagagccc tattaccgg aatctggatg ggaccgcctc cgggagctgt 350  
ttggcaaaga tgaacagcag agaatttcaa aggaccttgc taatatctgt 400  
aagacggcag ctacagcagg catcattggc tgggtgtatg ggggaatacc 450  
agcttttatt catgctaaac aacaatacat tgagcagagc caggcagaaa 500  
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cgaggcttca ttcgttatgg ctggcgctgg ggttgagaa ctgcagtgtt 600  
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acgctggtga gactgttcag gaaagaaaac agaaggatcg aaaggcactc 850  
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 ttaatctatc aatatatgca tacatggata tatccacca cctagatttt 1300  
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 t 1351

<210> 28

<211> 285

<212> PRT

<213> Homo sapiens

<400> 28

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Leu	Cys	Leu	Phe	Pro	Arg	Val	Phe	Ala	Ala	Glu	Ala	Val	Thr	Ala
				20					25					30

Asp	Ser	Glu	Val	Leu	Glu	Glu	Arg	Gln	Lys	Arg	Leu	Pro	Tyr	Val
				35					40					45

Pro	Glu	Pro	Tyr	Tyr	Pro	Glu	Ser	Gly	Trp	Asp	Arg	Leu	Arg	Glu
				50					55					60

Leu	Phe	Gly	Lys	Asp	Glu	Gln	Gln	Arg	Ile	Ser	Lys	Asp	Leu	Ala
				65					70					75

Asn	Ile	Cys	Lys	Thr	Ala	Ala	Thr	Ala	Gly	Ile	Ile	Gly	Trp	Val
				80					85					90

Tyr	Gly	Gly	Ile	Pro	Ala	Phe	Ile	His	Ala	Lys	Gln	Gln	Tyr	Ile
				95					100					105

Glu	Gln	Ser	Gln	Ala	Glu	Ile	Tyr	His	Asn	Arg	Phe	Asp	Ala	Val
				110					115					120

Gln	Ser	Ala	His	Arg	Ala	Ala	Thr	Arg	Gly	Phe	Ile	Arg	Tyr	Gly
				125					130					135

Trp	Arg	Trp	Gly	Trp	Arg	Thr	Ala	Val	Phe	Val	Thr	Ile	Phe	Asn
				140					145					150
Thr	Val	Asn	Thr	Ser	Leu	Asn	Val	Tyr	Arg	Asn	Lys	Asp	Ala	Leu
				155					160					165
Ser	His	Phe	Val	Ile	Ala	Gly	Ala	Val	Thr	Gly	Ser	Leu	Phe	Arg
				170					175					180
Ile	Asn	Val	Gly	Leu	Arg	Gly	Leu	Val	Ala	Gly	Gly	Ile	Ile	Gly
				185					190					195
Ala	Leu	Leu	Gly	Thr	Pro	Val	Gly	Gly	Leu	Leu	Met	Ala	Phe	Gln
				200					205					210
Lys	Tyr	Ala	Gly	Glu	Thr	Val	Gln	Glu	Arg	Lys	Gln	Lys	Asp	Arg
				215					220					225
Lys	Ala	Leu	His	Glu	Leu	Lys	Leu	Glu	Glu	Trp	Lys	Gly	Arg	Leu
				230					235					240
Gln	Val	Thr	Glu	His	Leu	Pro	Glu	Lys	Ile	Glu	Ser	Ser	Leu	Arg
				245					250					255
Glu	Asp	Glu	Pro	Glu	Asn	Asp	Ala	Lys	Lys	Ile	Glu	Ala	Leu	Leu
				260					265					270
Asn	Leu	Pro	Arg	Asn	Pro	Ser	Val	Ile	Asp	Lys	Gln	Asp	Lys	Asp
				275					280					285

<210> 29  
 <211> 324  
 <212> DNA  
 <213> Homo sapiens

<400> 29  
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 ctattaccgc gaatctggat gggaccgctc cgggagctgt ttggcaaaga 100  
 tgaacagcag agaatttcaa aggaccttgc taatatctgt aagacggcag 150  
 ctacagcagg catcattggc tgggtgtatg ggggaatacc agcttttatt 200  
 catgctaaac aacaatacat tgagcagagc caggcagaaa tttatcataa 250  
 ccggtttgat gctgtgcaat ctgcacatcg tgctgccaca cgaggcttca 300  
 ttcgttcatg gctggcgccg aacc 324

<210> 30  
 <211> 377  
 <212> DNA  
 <213> Homo sapiens

<220>

<221> unsure  
<222> 262, 330, 371  
<223> unknown base

<400> 30  
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gctgccgaag ctgtgactgc cgattcggaa gtccttgagg agcgtcagaa 150  
gcggcttccc tacgtcccag agccctatta cccggaattt ggatgggacc 200  
gcctccggga gctgtttggc aaagatgaac agcagagaat ttcaaaggac 250  
cttgctgata tntgtaagac ggcagctaca gcaggcatca ttggctgggt 300  
gtatggggga ataccagctt ttattcatgn taaacaaca tacattgagc 350  
agagccaggc agaaatttat nataacc 377

<210> 31  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 31  
tcgtacagtt acgctctccc 20

<210> 32  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 32  
cttgaggagc gtcagaagcg 20

<210> 33  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 33  
ataacgaatg aagcctcgtg 20

<210> 34  
<211> 40  
<212> DNA



<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 34

gctaatatct gtaagacggc agctacagca ggcatcattg 40

<210> 35

<211> 1819

<212> DNA

<213> Homo sapiens

<400> 35

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tgccggcaac cacaggttcc aagatggttt gcgggggctt cgcgtgttcc 200  
aagaactgcc tgtgcgccct caacctgctt tacaccttgg ttagtctgct 250  
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tccgagtggc cggcgtggtc attgcagtgg gcattcttctt gttcctgatt 350  
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tttttatatg attattctgt tacttgtatt tattgttcag ttttctgtat 450  
cttgcgcttg tttagccctg aaccaggagc aacagggtca gcttctggag 500  
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aaactgctgt gggttccgaa gtgttaacc aaatgacacc tgtctggcta 600  
gctgtgttaa aagtgaccac tcgtgtcgc catgtgctcc aatcatagga 650  
gaatatgctg gagaggtttt gagatttggt ggtggcattg gcctgttctt 700  
cagttttaca gagatcctgg gtgtttggct gacctacaga tacaggaacc 750  
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gaagatttcc tttcgtatta tgatcttggt cactttctgt aattttctgt 850  
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 atctcccata atttgaaatt gaaatcgtat tgtgtggctc tgtatattct 1750  
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<210> 36

<211> 204

<212> PRT

<213> Homo sapiens

<400> 36

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Leu	Asn	Leu	Leu	Tyr	Thr	Leu	Val	Ser	Leu	Leu	Leu	Ile	Gly	Ile
				20					25					30

Ala	Ala	Trp	Gly	Ile	Gly	Phe	Gly	Leu	Ile	Ser	Ser	Leu	Arg	Val
				35					40					45

Val	Gly	Val	Val	Ile	Ala	Val	Gly	Ile	Phe	Leu	Phe	Leu	Ile	Ala
				50					55					60

Leu	Val	Gly	Leu	Ile	Gly	Ala	Val	Lys	His	His	Gln	Val	Leu	Leu
				65					70					75

Phe	Phe	Tyr	Met	Ile	Ile	Leu	Leu	Leu	Val	Phe	Ile	Val	Gln	Phe
				80					85					90

Ser	Val	Ser	Cys	Ala	Cys	Leu	Ala	Leu	Asn	Gln	Glu	Gln	Gln	Gly
				95					100					105

Gln	Leu	Leu	Glu	Val	Gly	Trp	Asn	Asn	Thr	Ala	Ser	Ala	Arg	Asn	
				110					115					120	
Asp	Ile	Gln	Arg	Asn	Leu	Asn	Cys	Cys	Gly	Phe	Arg	Ser	Val	Asn	
				125					130					135	
Pro	Asn	Asp	Thr	Cys	Leu	Ala	Ser	Cys	Val	Lys	Ser	Asp	His	Ser	
				140					145					150	
Cys	Ser	Pro	Cys	Ala	Pro	Ile	Ile	Gly	Glu	Tyr	Ala	Gly	Glu	Val	
				155					160					165	
Leu	Arg	Phe	Val	Gly	Gly	Ile	Gly	Leu	Phe	Phe	Ser	Phe	Thr	Glu	
				170					175					180	
Ile	Leu	Gly	Val	Trp	Leu	Thr	Tyr	Arg	Tyr	Arg	Asn	Gln	Lys	Asp	
				185					190					195	
Pro	Arg	Ala	Asn	Pro	Ser	Ala	Phe	Leu							
				200											

<210> 37  
 <211> 390  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 20, 35, 61, 83, 106, 130, 133, 187, 232, 260, 336  
 <223> unknown base

<400> 37  
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 tattctgtaa nttgtattta ttgttcagtt ttntgtatct tgcgcttggt 100  
 tagccntgaa ccaggagcaa cagggtcagn ttntggaggt tggttggaac 150  
 aatacggcaa gtgctcgaaa tgacatccag agaaatntaa actgctgtgg 200  
 gttccgaagt gttaacccaa atgacacctg tntggctagc tgtgttaaaa 250  
 gtgaccactn gtgctcgcca tgtgctccaa tcataggaga atatgctgga 300  
 gaggttttga gatttggttg tggcattggc ctgttnttca gttttacaga 350  
 gatcctgggt gtttggctga cctacagata caggaaccag 390

<210> 38  
 <211> 566  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 27

<223> unknown base

<400> 38

aatcccaa at tccccaat ttttggnctt tttaggga gatgtgtgt 50  
ggtaaaaagt gttagtataa aaatgataat ttactttag tcttttatga 100  
ttacaccaat gtattctaga atagttatgt cttaggaaat tgtggtttaa 150  
tttttgactt ttacaggtaa gtgcaaagga gaagtgggtt catgaaatgt 200  
tctaattgat aataacattt accttcagcc tcccatcaga atggaacgag 250  
ttttgagtaa tccaggaagt atatctatat gatcttgata ttgttttata 300  
taatttgaag tctaaaagac tgcattttta aacaagttag tattaatgcg 350  
ttggcccacg tagcaaaaag atatttgatt atcttaaaaa ttgttaaata 400  
ccgttttcat gaaagtcttc agtattgtaa cagcaacttg tcaaacctaa 450  
gcatatttga atatgatctc ccataatttg aaattgaaat cgtattgtgt 500  
ggaggaaatg gcaatcttat gtgtgctgaa ggacacagta agagcaccaa 550  
gttgtgcccc acttgc 566

<210> 39

<211> 264

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 84-85, 206

<223> unknown base

<400> 39

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cttgtttagc ccctgaaacc aggagcaaca gggncagct tcctggaggt 100  
tggttgcaa caatcacggc caagtgactc cgcaaatgac atcccagaga 150  
aatcctaaac tgctgtgggt tccgaagtgt taacccaaat gacacctgtc 200  
tggctngctg tggtaaaagt gaccactcgt gctcgccatg tgctccaatc 250  
ataggagaat atgc 264

<210> 40

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 40  
acccacgtct gcgttgctgc c 21

<210> 41  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 41  
gagaatatgc tggagagg 18

<210> 42  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 42  
aggaatgcac taggattcgc gcgg 24

<210> 43  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 43  
ggccccaaag gcaaggacaa agcagctgtc agggaacctc cgccg 45

<210> 44  
<211> 2061  
<212> DNA  
<213> Homo sapiens

<400> 44  
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tcccttggtg tgctctgggt ggcccagatg ctactggctg ccagttttga 100  
gacgctgcag tgtgaggac ctgtctgcac tgaggagagc agctgccaca 150  
cggaggatga cttgactgat gcaagggaag ctggcttcca ggtcaaggcc 200  
tacactttca gtgaaccctt ccacctgatt gtgtcctatg actggetgat 250  
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gctgccaggc ctggcaagac tggccactga ctcaggtgac cttctaccga 350

gatggctcag ctctgggtcc ccccgggcct aacagggaat tctccatcac 400  
cgtggtacaa aaggcagaca gcgggcacta ccactgcagt ggcatcttcc 450  
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gtccaagaac tgtttccagc gccaatctc agagctgtac cctcagctga 550  
acccaagca ggaagcccca tgaccctgag ttgtcagaca aagttgcccc 600  
tgcagaggtc agctgcccgc ctctcttct cttctacaa ggatggaagg 650  
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agaagatcac tccgggtcat actggtgtga ggcagccact gaggacaacc 750  
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agaattagag ttagctata attgtgtatt ctctctaac acaacagaat 1300  
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ggtgatggca ttaagaagtg ggcctttggg aagtgattag atcaggagtg 1850  
 cagagccctc atgattagga ttagtgcctt tatttaaaaa ggccccagag 1900  
 agctaactca cccttcacc atatgaggac gtggcaagaa gatgacatgt 1950  
 atgagaacca aaaaacagct gtcgccaaac accgactctg tcgttgctt 2000  
 gatcttgaac ttccagcctc cagaactatg agaaataaaa ttctggttgt 2050  
 ttgtagccta a 2061

<210> 45  
 <211> 359  
 <212> PRT  
 <213> Homo sapiens

<400> 45  
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 Leu Gly Val Leu Trp Val Ala Gln Met Leu Leu Ala Ala Ser Phe  
 20 25 30  
 Glu Thr Leu Gln Cys Glu Gly Pro Val Cys Thr Glu Glu Ser Ser  
 35 40 45  
 Cys His Thr Glu Asp Asp Leu Thr Asp Ala Arg Glu Ala Gly Phe  
 50 55 60  
 Gln Val Lys Ala Tyr Thr Phe Ser Glu Pro Phe His Leu Ile Val  
 65 70 75  
 Ser Tyr Asp Trp Leu Ile Leu Gln Gly Pro Ala Lys Pro Val Phe  
 80 85 90  
 Glu Gly Asp Leu Leu Val Leu Arg Cys Gln Ala Trp Gln Asp Trp  
 95 100 105  
 Pro Leu Thr Gln Val Thr Phe Tyr Arg Asp Gly Ser Ala Leu Gly  
 110 115 120  
 Pro Pro Gly Pro Asn Arg Glu Phe Ser Ile Thr Val Val Gln Lys  
 125 130 135  
 Ala Asp Ser Gly His Tyr His Cys Ser Gly Ile Phe Gln Ser Pro  
 140 145 150  
 Gly Pro Gly Ile Pro Glu Thr Ala Ser Val Val Ala Ile Thr Val  
 155 160 165  
 Gln Glu Leu Phe Pro Ala Pro Ile Leu Arg Ala Val Pro Ser Ala  
 170 175 180  
 Glu Pro Gln Ala Gly Ser Pro Met Thr Leu Ser Cys Gln Thr Lys  
 185 190 195

Leu	Pro	Leu	Gln	Arg	Ser	Ala	Ala	Arg	Leu	Leu	Phe	Ser	Phe	Tyr	200	205	210
Lys	Asp	Gly	Arg	Ile	Val	Gln	Ser	Arg	Gly	Leu	Ser	Ser	Glu	Phe	215	220	225
Gln	Ile	Pro	Thr	Ala	Ser	Glu	Asp	His	Ser	Gly	Ser	Tyr	Trp	Cys	230	235	240
Glu	Ala	Ala	Thr	Glu	Asp	Asn	Gln	Val	Trp	Lys	Gln	Ser	Pro	Gln	245	250	255
Leu	Glu	Ile	Arg	Val	Gln	Gly	Ala	Ser	Ser	Ser	Ala	Ala	Pro	Pro	260	265	270
Thr	Leu	Asn	Pro	Ala	Pro	Gln	Lys	Ser	Ala	Ala	Pro	Gly	Thr	Ala	275	280	285
Pro	Glu	Glu	Ala	Pro	Gly	Pro	Leu	Pro	Pro	Pro	Pro	Thr	Pro	Ser	290	295	300
Ser	Glu	Asp	Pro	Gly	Phe	Ser	Ser	Pro	Leu	Gly	Met	Pro	Asp	Pro	305	310	315
His	Leu	Tyr	His	Gln	Met	Gly	Leu	Leu	Leu	Lys	His	Met	Gln	Asp	320	325	330
Val	Arg	Val	Leu	Leu	Gly	His	Leu	Leu	Met	Glu	Leu	Arg	Glu	Leu	335	340	345
Ser	Gly	His	Gln	Lys	Pro	Gly	Thr	Thr	Lys	Ala	Thr	Ala	Glu		350	355	

<210> 46

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 46

tgggctgtgt cctcatgg 18

<210> 47

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 47

tttcagcgc caattctc 18

<210> 48



<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 48  
agttcttgga ctgtgatagc cac 23

<210> 49  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 49  
aaacttggtt gtcctcagtg gctg 24

<210> 50  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 50  
gtgagggacc tgtctgcact gaggagagca gctgccacac ggagg 45

<210> 51  
<211> 2181  
<212> DNA  
<213> Homo sapiens

<400> 51  
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ccaccagaag tttgagcctc tttggtagca ggaggctgga agaaaggaca 100  
gaagtagctc tggctgtgat ggggatctta ctgggcctgc tactcctggg 150  
gcacctaaca gtggacactt atggccgtcc catcctggaa gtgccagaga 200  
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ctcagaccct gtcaccatct ttctacgtga ctcttctgga gaccatatcc 350  
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gatgtatccc tccaattgag caccctggag atggatgacc ggagccacta 450  
cacgtgtgaa gtcacctggc agactcctga tggcaaccaa gtcgtgagag 500

ataagattac tgagctccgt gtccagaaac tctctgtctc caagcccaca 550  
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accttactct tcaagcctgc ggtgatagcc gactcaggct cctatttctg 750  
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acaaccatga catacccctt gaaagcaaca tctacagtga agcagtcctg 900  
ggactggacc actgacatgg atggctacct tggagagacc agtgctgggc 950  
caggaaagag cctgcctgtc ttgccatca tctcatcat ctccttgtgc 1000  
tgtatgggtg tttttaccat ggcctatata atgctctgtc ggaagacatc 1050  
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 aggctcagct ctgccagctc agaggaccag ctatatccag gatcatttct 2050  
 ctttcttcag ggccagacag cttttaattg aaattgttat ttcacaggcc 2100  
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 tgggtgctcaa taaatatcta atcataacag c 2181

<210> 52  
 <211> 321  
 <212> PRT  
 <213> Homo sapiens

<400> 52  
 Met Gly Ile Leu Leu Gly Leu Leu Leu Leu Gly His Leu Thr Val  
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 20 25 30  
 Gly Pro Trp Lys Gly Asp Val Asn Leu Pro Cys Thr Tyr Asp Pro  
 35 40 45  
 Leu Gln Gly Tyr Thr Gln Val Leu Val Lys Trp Leu Val Gln Arg  
 50 55 60  
 Gly Ser Asp Pro Val Thr Ile Phe Leu Arg Asp Ser Ser Gly Asp  
 65 70 75  
 His Ile Gln Gln Ala Lys Tyr Gln Gly Arg Leu His Val Ser His  
 80 85 90  
 Lys Val Pro Gly Asp Val Ser Leu Gln Leu Ser Thr Leu Glu Met  
 95 100 105  
 Asp Asp Arg Ser His Tyr Thr Cys Glu Val Thr Trp Gln Thr Pro  
 110 115 120  
 Asp Gly Asn Gln Val Val Arg Asp Lys Ile Thr Glu Leu Arg Val  
 125 130 135  
 Gln Lys Leu Ser Val Ser Lys Pro Thr Val Thr Thr Gly Ser Gly  
 140 145 150  
 Tyr Gly Phe Thr Val Pro Gln Gly Met Arg Ile Ser Leu Gln Cys  
 155 160 165  
 Gln Ala Arg Gly Ser Pro Pro Ile Ser Tyr Ile Trp Tyr Lys Gln  
 170 175 180  
 Gln Thr Asn Asn Gln Glu Pro Ile Lys Val Ala Thr Leu Ser Thr  
 185 190 195

Leu	Leu	Phe	Lys	Pro	Ala	Val	Ile	Ala	Asp	Ser	Gly	Ser	Tyr	Phe	200	205	210
Cys	Thr	Ala	Lys	Gly	Gln	Val	Gly	Ser	Glu	Gln	His	Ser	Asp	Ile	215	220	225
Val	Lys	Phe	Val	Val	Lys	Asp	Ser	Ser	Lys	Leu	Leu	Lys	Thr	Lys	230	235	240
Thr	Glu	Ala	Pro	Thr	Thr	Met	Thr	Tyr	Pro	Leu	Lys	Ala	Thr	Ser	245	250	255
Thr	Val	Lys	Gln	Ser	Trp	Asp	Trp	Thr	Thr	Asp	Met	Asp	Gly	Tyr	260	265	270
Leu	Gly	Glu	Thr	Ser	Ala	Gly	Pro	Gly	Lys	Ser	Leu	Pro	Val	Phe	275	280	285
Ala	Ile	Ile	Leu	Ile	Ile	Ser	Leu	Cys	Cys	Met	Val	Val	Phe	Thr	290	295	300
Met	Ala	Tyr	Ile	Met	Leu	Cys	Arg	Lys	Thr	Ser	Gln	Gln	Glu	His	305	310	315
Val	Tyr	Glu	Ala	Ala	Arg										320		

<210> 53  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 53  
 tatccoctcca attgagcacc ctgg 24

<210> 54  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 54  
 gtcggaagac atcccaacaa g 21

<210> 55  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 55

cttcacaatg tcgctgtgct gctc 24

<210> 56

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 56

agccaaatcc agcagctggc ttac 24

<210> 57

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 57

tggatgaccg gagccactac acgtgtgaag tcacctggca gactcctgat 50

<210> 58

<211> 2458

<212> DNA

<213> Homo sapiens

<400> 58

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 <213> Homo sapiens

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 Thr Glu Glu Gln Lys Gly Arg Val Ala Phe Ala Ser Asn Phe Leu  
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 Ala Gly Asp Ala Ser Leu Gln Ile Glu Pro Leu Lys Pro Ser Asp  
                   95                  100                  105  
 Glu Gly Arg Tyr Thr Cys Lys Val Lys Asn Ser Gly Arg Tyr Val  
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 Trp Ser His Val Ile Leu Lys Val Leu Val Arg Pro Ser Lys Pro  
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 Lys Cys Glu Leu Glu Gly Glu Leu Thr Glu Gly Ser Asp Leu Thr  
                   140                  145                  150  
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 Trp Gln Arg Ile Arg Glu Lys Glu Gly Glu Asp Glu Arg Leu Pro

	170	175	180
Pro Lys Ser Arg	Ile Asp Tyr Asn His 185	Pro Gly Arg Val Leu 190	Leu 195
Gln Asn Leu Thr	Met Ser Tyr Ser Gly 200	Leu Tyr Gln Cys Thr 205	Ala 210
Gly Asn Glu Ala	Gly Lys Glu Ser Cys 215	Val Val Arg Val Thr 220	Val 225
Gln Tyr Val Gln	Ser Ile Gly Met Val 230	Ala Gly Ala Val Thr 235	Gly 240
Ile Val Ala Gly	Ala Leu Leu Ile Phe 245	Leu Leu Val Trp Leu 250	Leu 255
Ile Arg Arg Lys	Asp Lys Glu Arg Tyr 260	Glu Glu Glu Glu Arg 265	Pro 270
Asn Glu Ile Arg	Glu Asp Ala Glu Ala 275	Pro Lys Ala Arg Leu 280	Val 285
Lys Pro Ser Ser	Ser Ser Ser Gly Ser 290	Arg Ser Ser Arg Ser 295	Gly 300
Ser Ser Ser Thr	Arg Ser Thr Ala Asn 305	Ser Ala Ser Arg Ser 310	Gln 315
Arg Thr Leu Ser	Thr Asp Ala Ala Pro 320	Gln Pro Gly Leu Ala 325	Thr 330
Gln Ala Tyr Ser	Leu Val Gly Pro Glu 335	Val Arg Gly Ser Glu 340	Pro 345
Lys Lys Val His	His Ala Asn Leu Thr 350	Lys Ala Glu Thr Thr 355	Pro 360
Ser Met Ile Pro	Ser Gln Ser Arg Ala 365	Phe Gln Thr Val 370	

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<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 60

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<210> 61

<211> 24

<212> DNA

<213> Artificial Sequence



<220>

<223> Synthetic oligonucleotide probe

<400> 61

actaggctgt atgcctgggt gggc 24

<210> 62

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 62

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<210> 63

<211> 3534

<212> DNA

<213> Homo sapiens

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<211> 655

<212> PRT

<213> Homo sapiens

<400> 64

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Leu	Leu	Leu	Gly	Phe	Leu	Ser	Thr	Thr	Thr	Ala	Gln	Pro	Glu	Gln	35	40	45	
Lys	Ala	Ser	Asn	Leu	Ile	Gly	Thr	Tyr	Arg	His	Val	Asp	Arg	Ala	50	55	60	
Thr	Gly	Gln	Val	Leu	Thr	Cys	Asp	Lys	Cys	Pro	Ala	Gly	Thr	Tyr	65	70	75	
Val	Ser	Glu	His	Cys	Thr	Asn	Thr	Ser	Leu	Arg	Val	Cys	Ser	Ser	80	85	90	
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Cys	His	Asp	Cys	Ser	Gln	Pro	Cys	Pro	Trp	Pro	Met	Ile	Glu	Lys	110	115	120	
Leu	Pro	Cys	Ala	Ala	Leu	Thr	Asp	Arg	Glu	Cys	Thr	Cys	Pro	Pro	125	130	135	
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Pro	Val	Gly	Trp	Gly	Val	Arg	Lys	Lys	Gly	Thr	Glu	Thr	Glu	Asp	155	160	165	
Val	Arg	Cys	Lys	Gln	Cys	Ala	Arg	Gly	Thr	Phe	Ser	Asp	Val	Pro	170	175	180	
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Cys	Gly	Thr	Leu	Pro	Ser	Phe	Ser	Ser	Ser	Thr	Ser	Pro	Ser	Pro	215	220	225	
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Val	Pro	Ser	Ser	Thr	Tyr	Val	Pro	Lys	Gly	Met	Asn	Ser	Thr	Glu	245	250	255	
Ser	Asn	Ser	Ser	Ala	Ser	Val	Arg	Pro	Lys	Val	Leu	Ser	Ser	Ile	260	265	270	
Gln	Glu	Gly	Thr	Val	Pro	Asp	Asn	Thr	Ser	Ser	Ala	Arg	Gly	Lys	275	280	285	

Glu	Asp	Val	Asn	Lys	Thr	Leu	Pro	Asn	Leu	Gln	Val	Val	Asn	His	290	295	300
Gln	Gln	Gly	Pro	His	His	Arg	His	Ile	Leu	Lys	Leu	Leu	Pro	Ser	305	310	315
Met	Glu	Ala	Thr	Gly	Gly	Glu	Lys	Ser	Ser	Thr	Pro	Ile	Lys	Gly	320	325	330
Pro	Lys	Arg	Gly	His	Pro	Arg	Gln	Asn	Leu	His	Lys	His	Phe	Asp	335	340	345
Ile	Asn	Glu	His	Leu	Pro	Trp	Met	Ile	Val	Leu	Phe	Leu	Leu	Leu	350	355	360
Val	Leu	Val	Val	Ile	Val	Val	Cys	Ser	Ile	Arg	Lys	Ser	Ser	Arg	365	370	375
Thr	Leu	Lys	Lys	Gly	Pro	Arg	Gln	Asp	Pro	Ser	Ala	Ile	Val	Glu	380	385	390
Lys	Ala	Gly	Leu	Lys	Lys	Ser	Met	Thr	Pro	Thr	Gln	Asn	Arg	Glu	395	400	405
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Gly	Leu	Met	Glu	Asp	Thr	Thr	Gln	Leu	Glu	Thr	Asp	Lys	Leu	Ala	500	505	510
Leu	Pro	Met	Ser	Pro	Ser	Pro	Leu	Ser	Pro	Ser	Pro	Ile	Pro	Ser	515	520	525
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Ser	Pro	Gln	Asp	Lys	Asn	Lys	Gly	Phe	Phe	Val	Asp	Glu	Ser	Glu	545	550	555
Pro	Leu	Leu	Arg	Cys	Asp	Ser	Thr	Ser	Ser	Gly	Ser	Ser	Ala	Leu	560	565	570

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Asp	Asp	Met	Leu	His	Phe	Leu	Asn	Pro	Glu	Glu	Leu	Arg	Val	Ile
				605					610					615
Glu	Glu	Ile	Pro	Gln	Ala	Glu	Asp	Lys	Leu	Asp	Arg	Leu	Phe	Glu
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Ile	Ile	Gly	Val	Lys	Ser	Gln	Glu	Ala	Ser	Gln	Thr	Leu	Leu	Asp
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Ser	Val	Tyr	Ser	His	Leu	Pro	Asp	Leu	Leu					
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<210> 68  
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<400> 68

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atttggtgct tgacgtatta ttgtcctttg attccaaata atatgtttcc 2350  
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catccactga aa 2412

<210> 69  
<211> 453  
<212> PRT  
<213> Homo sapiens

<400> 69  
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Arg Ser Leu Phe Gly Leu Asp Asp Leu Lys Ile Ser Pro Val Ala  
20 25 30  
Pro Asp Ala Asp Ala Val Ala Ala Gln Ile Leu Ser Leu Leu Pro  
35 40 45  
Leu Lys Phe Phe Pro Ile Ile Val Ile Gly Ile Ile Ala Leu Ile



50					55					60				
Leu	Ala	Leu	Ala	Ile	Gly	Leu	Gly	Ile	His	Phe	Asp	Cys	Ser	Gly
				65					70					75
Lys	Tyr	Arg	Cys	Arg	Ser	Ser	Phe	Lys	Cys	Ile	Glu	Leu	Ile	Ala
				80					85					90
Arg	Cys	Asp	Gly	Val	Ser	Asp	Cys	Lys	Asp	Gly	Glu	Asp	Glu	Tyr
				95					100					105
Arg	Cys	Val	Arg	Val	Gly	Gly	Gln	Asn	Ala	Val	Leu	Gln	Val	Phe
				110					115					120
Thr	Ala	Ala	Ser	Trp	Lys	Thr	Met	Cys	Ser	Asp	Asp	Trp	Lys	Gly
				125					130					135
His	Tyr	Ala	Asn	Val	Ala	Cys	Ala	Gln	Leu	Gly	Phe	Pro	Ser	Tyr
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Val	Ser	Ser	Asp	Asn	Leu	Arg	Val	Ser	Ser	Leu	Glu	Gly	Gln	Phe
				155					160					165
Arg	Glu	Glu	Phe	Val	Ser	Ile	Asp	His	Leu	Leu	Pro	Asp	Asp	Lys
				170					175					180
Val	Thr	Ala	Leu	His	His	Ser	Val	Tyr	Val	Arg	Glu	Gly	Cys	Ala
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Ser	Gly	His	Val	Val	Thr	Leu	Gln	Cys	Thr	Ala	Cys	Gly	His	Arg
				200					205					210
Arg	Gly	Tyr	Ser	Ser	Arg	Ile	Val	Gly	Gly	Asn	Met	Ser	Leu	Leu
				215					220					225
Ser	Gln	Trp	Pro	Trp	Gln	Ala	Ser	Leu	Gln	Phe	Gln	Gly	Tyr	His
				230					235					240
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Ala	His	Cys	Val	Tyr	Asp	Leu	Tyr	Leu	Pro	Lys	Ser	Trp	Thr	Ile
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Gln	Val	Gly	Leu	Val	Ser	Leu	Leu	Asp	Asn	Pro	Ala	Pro	Ser	His
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Leu	Val	Glu	Lys	Ile	Val	Tyr	His	Ser	Lys	Tyr	Lys	Pro	Lys	Arg
				290					295					300
Leu	Gly	Asn	Asp	Ile	Ala	Leu	Met	Lys	Leu	Ala	Gly	Pro	Leu	Thr
				305					310					315
Phe	Asn	Glu	Met	Ile	Gln	Pro	Val	Cys	Leu	Pro	Asn	Ser	Glu	Glu
				320					325					330
Asn	Phe	Pro	Asp	Gly	Lys	Val	Cys	Trp	Thr	Ser	Gly	Trp	Gly	Ala

	335	340	345
Thr Glu Asp Gly	Gly Asp Ala Ser Pro	Val Leu Asn His Ala	Ala
	350	355	360
Val Pro Leu Ile	Ser Asn Lys Ile Cys	Asn His Arg Asp Val	Tyr
	365	370	375
Gly Gly Ile Ile	Ser Pro Ser Met Leu	Cys Ala Gly Tyr Leu	Thr
	380	385	390
Gly Gly Val Asp	Ser Cys Gln Gly Asp	Ser Gly Gly Pro Leu	Val
	395	400	405
Cys Gln Glu Arg	Arg Leu Trp Lys Leu	Val Gly Ala Thr Ser	Phe
	410	415	420
Gly Ile Gly Cys	Ala Glu Val Asn Lys	Pro Gly Val Tyr Thr	Arg
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Val Thr Ser Phe	Leu Asp Trp Ile His	Glu Gln Met Glu Arg	Asp
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Leu Lys Thr

<210> 70

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 70

tgacatcgcc cttatgaagc tggc 24

<210> 71

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 71

tacacgtccc tgtggttgca gatc 24

<210> 72

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 72

cgttcaatgc agaaatgata cagcctgtgt gcctgcccaa ctctgaagag 50

<210> 73

<211> 3305

<212> DNA

<213> Homo sapiens

<400> 73

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gcacgcacac acacgggggg aaactttttt aaaaatgaaa ggctagaaga 150  
gctcagcggc ggcgcggggc ctgcgcgagg gctccggagc tgactcgccg 200  
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caacccttca ttttaacaagt aagaatgtta aaaagtgaaa acaatgtaag 3250  
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gaaat 3305

<210> 74  
<211> 735  
<212> PRT  
<213> Homo sapiens

<400> 74  
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20 25 30  
Val Ser Leu Trp Asn Gln Gly Arg Ala Asp Glu Val Val Ser Ala  
35 40 45  
Ser Val Arg Ser Gly Asp Leu Trp Ile Pro Val Lys Ser Phe Asp  
50 55 60  
Ser Lys Asn His Pro Glu Val Leu Asn Ile Arg Leu Gln Arg Glu  
65 70 75  
Ser Lys Glu Leu Ile Ile Asn Leu Glu Arg Asn Glu Gly Leu Ile  
80 85 90  
Ala Ser Ser Phe Thr Glu Thr His Tyr Leu Gln Asp Gly Thr Asp  
95 100 105  
Val Ser Leu Ala Arg Asn Tyr Thr Gly His Cys Tyr Tyr His Gly  
110 115 120

His Val Arg Gly Tyr Ser Asp Ser Ala Val Ser Leu Ser Thr Cys	125	130	135
Ser Gly Leu Arg Gly Leu Ile Val Phe Glu Asn Glu Ser Tyr Val	140	145	150
Leu Glu Pro Met Lys Ser Ala Thr Asn Arg Tyr Lys Leu Phe Pro	155	160	165
Ala Lys Lys Leu Lys Ser Val Arg Gly Ser Cys Gly Ser His His	170	175	180
Asn Thr Pro Asn Leu Ala Ala Lys Asn Val Phe Pro Pro Pro Ser	185	190	195
Gln Thr Trp Ala Arg Arg His Lys Arg Glu Thr Leu Lys Ala Thr	200	205	210
Lys Tyr Val Glu Leu Val Ile Val Ala Asp Asn Arg Glu Phe Gln	215	220	225
Arg Gln Gly Lys Asp Leu Glu Lys Val Lys Gln Arg Leu Ile Glu	230	235	240
Ile Ala Asn His Val Asp Lys Phe Tyr Arg Pro Leu Asn Ile Arg	245	250	255
Ile Val Leu Val Gly Val Glu Val Trp Asn Asp Met Asp Lys Cys	260	265	270
Ser Val Ser Gln Asp Pro Phe Thr Ser Leu His Glu Phe Leu Asp	275	280	285
Trp Arg Lys Met Lys Leu Leu Pro Arg Lys Ser His Asp Asn Ala	290	295	300
Gln Leu Val Ser Gly Val Tyr Phe Gln Gly Thr Thr Ile Gly Met	305	310	315
Ala Pro Ile Met Ser Met Cys Thr Ala Asp Gln Ser Gly Gly Ile	320	325	330
Val Met Asp His Ser Asp Asn Pro Leu Gly Ala Ala Val Thr Leu	335	340	345
Ala His Glu Leu Gly His Asn Phe Gly Met Asn His Asp Thr Leu	350	355	360
Asp Arg Gly Cys Ser Cys Gln Met Ala Val Glu Lys Gly Gly Cys	365	370	375
Ile Met Asn Ala Ser Thr Gly Tyr Pro Phe Pro Met Val Phe Ser	380	385	390
Ser Cys Ser Arg Lys Asp Leu Glu Thr Ser Leu Glu Lys Gly Met	395	400	405

Gly	Val	Cys	Leu	Phe	Asn	Leu	Pro	Glu	Val	Arg	Glu	Ser	Phe	Gly	410	415	420
Gly	Gln	Lys	Cys	Gly	Asn	Arg	Phe	Val	Glu	Glu	Gly	Glu	Glu	Cys	425	430	435
Asp	Cys	Gly	Glu	Pro	Glu	Glu	Cys	Met	Asn	Arg	Cys	Cys	Asn	Ala	440	445	450
Thr	Thr	Cys	Thr	Leu	Lys	Pro	Asp	Ala	Val	Cys	Ala	His	Gly	Leu	455	460	465
Cys	Cys	Glu	Asp	Cys	Gln	Leu	Lys	Pro	Ala	Gly	Thr	Ala	Cys	Arg	470	475	480
Asp	Ser	Ser	Asn	Ser	Cys	Asp	Leu	Pro	Glu	Phe	Cys	Thr	Gly	Ala	485	490	495
Ser	Pro	His	Cys	Pro	Ala	Asn	Val	Tyr	Leu	His	Asp	Gly	His	Ser	500	505	510
Cys	Gln	Asp	Val	Asp	Gly	Tyr	Cys	Tyr	Asn	Gly	Ile	Cys	Gln	Thr	515	520	525
His	Glu	Gln	Gln	Cys	Val	Thr	Leu	Trp	Gly	Pro	Gly	Ala	Lys	Pro	530	535	540
Ala	Pro	Gly	Ile	Cys	Phe	Glu	Arg	Val	Asn	Ser	Ala	Gly	Asp	Pro	545	550	555
Tyr	Gly	Asn	Cys	Gly	Lys	Val	Ser	Lys	Ser	Ser	Phe	Ala	Lys	Cys	560	565	570
Glu	Met	Arg	Asp	Ala	Lys	Cys	Gly	Lys	Ile	Gln	Cys	Gln	Gly	Gly	575	580	585
Ala	Ser	Arg	Pro	Val	Ile	Gly	Thr	Asn	Ala	Val	Ser	Ile	Glu	Thr	590	595	600
Asn	Ile	Pro	Leu	Gln	Gln	Gly	Gly	Arg	Ile	Leu	Cys	Arg	Gly	Thr	605	610	615
His	Val	Tyr	Leu	Gly	Asp	Asp	Met	Pro	Asp	Pro	Gly	Leu	Val	Leu	620	625	630
Ala	Gly	Thr	Lys	Cys	Ala	Asp	Gly	Lys	Ile	Cys	Leu	Asn	Arg	Gln	635	640	645
Cys	Gln	Asn	Ile	Ser	Val	Phe	Gly	Val	His	Glu	Cys	Ala	Met	Gln	650	655	660
Cys	His	Gly	Arg	Gly	Val	Cys	Asn	Asn	Arg	Lys	Asn	Cys	His	Cys	665	670	675
Glu	Ala	His	Trp	Ala	Pro	Pro	Phe	Cys	Asp	Lys	Phe	Gly	Phe	Gly	680	685	690

Gly Ser Thr Asp Ser Gly Pro Ile Arg Gln Ala Glu Ala Arg Gln  
695 700 705

Glu Ala Ala Glu Ser Asn Arg Glu Arg Gly Gln Gly Gln Glu Pro  
710 715 720

Val Gly Ser Gln Glu His Ala Ser Thr Ala Ser Leu Thr Leu Ile  
725 730 735

<210> 75

<211> 483

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 30, 94, 143, 156, 163, 179, 193, 369, 371, 381, 390, 473

<223> unknown base

<400> 75

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ctaccagga agtttgaga aacagtgcga ggaagggcag ganttcctgg 150

ttgagntttt tgntaaaaca tggacatgnt tcagtgtgc tcntgagaga 200

gtagcagggtt accacttttg gcaggcccca gccctgcagc aaggaggaag 250

aggactcaaa agtttggcct ttcactgagc ctccacagca gtgggggaga 300

agcaagggtt gggcccagtg tcccctttcc ccagtgcac ctcagccttg 350

gcagccctga taactggtnt ntggctgcaa nttaatgctn tgatatggct 400

tttagcattht attatatgaa aatagcaggg ttttagtttt taatttatca 450

gagaccctgc caccattcc atntccatcc aag 483

<210> 76

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 76

gtctcagcac gtgttctggt ctcaggg 27

<210> 77

<211> 18

<212> DNA

<213> Artificial Sequence



<220>  
<223> Synthetic oligonucleotide probe

<400> 77  
catgagcatg tgcacggc 18

<210> 78  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 78  
tacctgcacg atgggcac 18

<210> 79  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 79  
cactgggcac ctcccttc 18

<210> 80  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
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<400> 80  
ctccaggctg gtctccaagt ccttcc 26

<210> 81  
<211> 24  
<212> DNA  
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<400> 81  
tccctgttg actctgcagc ttcc 24

<210> 82  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 82  
cttcgctggg aagagtttg 19

<210> 83  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 83  
gtgcaaccaa cagatacaaa ctcttcccag cgaagaagct gaaaagcgtc 50 .

<210> 84  
<211> 1714  
<212> DNA  
<213> Homo sapiens

<400> 84  
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atgatctgcc cgcctcggcc tcccaaagtg ctgggattac aggcgagtgc 150  
  
aaccacaccc ggccacaaac tttttaagaa gttaatgaaa ccataccttt 200  
  
tacattttta atgacaggaa aatgctcaca ataattgtta acccaaaatt 250  
  
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tatgaaaata taccaaatat caataatact tatctctggg taaaaacctc 350  
  
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agggaaaaat cacgccactt gggaaaaaaa gattcgaaat ctgccttttt 500  
  
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<210> 85
<211> 67
<212> PRT
<213> Homo sapiens

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             20             25             30

Thr Ser Met Pro Glu Ala Thr Ala Ala Glu Thr Thr Lys Pro Ser
             35             40             45

Asn Ser Ala Leu Gln Pro Thr Ala Gly Leu Leu Val Val Leu Leu
             50             55             60

Ala Leu Leu His Leu Tyr His
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<210> 86
<211> 23

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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 86  
acgggcacac tggatcccaa atg 23

<210> 87  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 87  
ggtagagatg tagaaggga agcaagacc 29

<210> 88  
<211> 50  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 88  
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<210> 89  
<211> 2956  
<212> DNA  
<213> Homo sapiens

<400> 89  
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 <211> 432  
 <212> PRT  
 <213> Homo sapiens

<400> 90  
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 20 25 30  
 Gly Gly Arg Trp Gly Ala Arg Ala Gln Glu Ala Ala Ala Ala Ala  
 35 40 45

Ala	Asp	Gly	Pro	Pro	Ala	Ala	Asp	Gly	Glu	Asp	Gly	Gln	Asp	Pro			
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His	Ser	Lys	His	Leu	Tyr	Thr	Ala	Asp	Met	Phe	Thr	His	Gly	Ile			
				65					70					75			
Gln	Ser	Ala	Ala	His	Phe	Val	Met	Phe	Phe	Ala	Pro	Trp	Cys	Gly			
				80					85					90			
His	Cys	Gln	Arg	Leu	Gln	Pro	Thr	Trp	Asn	Asp	Leu	Gly	Asp	Lys			
				95					100					105			
Tyr	Asn	Ser	Met	Glu	Asp	Ala	Lys	Val	Tyr	Val	Ala	Lys	Val	Asp			
				110					115					120			
Cys	Thr	Ala	His	Ser	Asp	Val	Cys	Ser	Ala	Gln	Gly	Val	Arg	Gly			
				125					130					135			
Tyr	Pro	Thr	Leu	Lys	Leu	Phe	Lys	Pro	Gly	Gln	Glu	Ala	Val	Lys			
				140					145					150			
Tyr	Gln	Gly	Pro	Arg	Asp	Phe	Gln	Thr	Leu	Glu	Asn	Trp	Met	Leu			
				155					160					165			
Gln	Thr	Leu	Asn	Glu	Glu	Pro	Val	Thr	Pro	Glu	Pro	Glu	Val	Glu			
				170					175					180			
Pro	Pro	Ser	Ala	Pro	Glu	Leu	Lys	Gln	Gly	Leu	Tyr	Glu	Leu	Ser			
				185					190					195			
Ala	Ser	Asn	Phe	Glu	Leu	His	Val	Ala	Gln	Gly	Asp	His	Phe	Ile			
				200					205					210			
Lys	Phe	Phe	Ala	Pro	Trp	Cys	Gly	His	Cys	Lys	Ala	Leu	Ala	Pro			
				215					220					225			
Thr	Trp	Glu	Gln	Leu	Ala	Leu	Gly	Leu	Glu	His	Ser	Glu	Thr	Val			
				230					235					240			
Lys	Ile	Gly	Lys	Val	Asp	Cys	Thr	Gln	His	Tyr	Glu	Leu	Cys	Ser			
				245					250					255			
Gly	Asn	Gln	Val	Arg	Gly	Tyr	Pro	Thr	Leu	Leu	Trp	Phe	Arg	Asp			
				260					265					270			
Gly	Lys	Lys	Val	Asp	Gln	Tyr	Lys	Gly	Lys	Arg	Asp	Leu	Glu	Ser			
				275					280					285			
Leu	Arg	Glu	Tyr	Val	Glu	Ser	Gln	Leu	Gln	Arg	Thr	Glu	Thr	Gly			
				290					295					300			
Ala	Thr	Glu	Thr	Val	Thr	Pro	Ser	Glu	Ala	Pro	Val	Leu	Ala	Ala			
				305					310					315			
Glu	Pro	Glu	Ala	Asp	Lys	Gly	Thr	Val	Leu	Ala	Leu	Thr	Glu	Asn			
				320					325					330			

Asn	Phe	Asp	Asp	Thr	Ile	Ala	Glu	Gly	Ile	Thr	Phe	Ile	Lys	Phe	
				335					340					345	
Tyr	Ala	Pro	Trp	Cys	Gly	His	Cys	Lys	Thr	Leu	Ala	Pro	Thr	Trp	
				350					355					360	
Glu	Glu	Leu	Ser	Lys	Lys	Glu	Phe	Pro	Gly	Leu	Ala	Gly	Val	Lys	
				365					370					375	
Ile	Ala	Glu	Val	Asp	Cys	Thr	Ala	Glu	Arg	Asn	Ile	Cys	Ser	Lys	
				380					385					390	
Tyr	Ser	Val	Arg	Gly	Tyr	Pro	Thr	Leu	Leu	Leu	Phe	Arg	Gly	Gly	
				395					400					405	
Lys	Lys	Val	Ser	Glu	His	Ser	Gly	Gly	Arg	Asp	Leu	Asp	Ser	Leu	
				410					415					420	
His	Arg	Phe	Val	Leu	Ser	Gln	Ala	Lys	Asp	Glu	Leu				
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 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

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<210> 92  
 <211> 21  
 <212> DNA  
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<220>  
 <223> Synthetic oligonucleotide probe

<400> 92  
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<210> 93  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
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<210> 94  
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<212> DNA  
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<220>  
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<400> 94  
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<210> 95  
<211> 49  
<212> DNA  
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<220>  
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<400> 95  
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<210> 96  
<211> 1016  
<212> DNA  
<213> Homo sapiens

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<210> 97  
 <211> 277  
 <212> PRT  
 <213> Homo sapiens

<400> 97  
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 Asp Ser Arg Pro Thr Ala Glu Val Cys Ala Thr His Thr Ile Ser  
 35 40 45  
 Pro Gly Pro Lys Gly Asp Asp Gly Glu Lys Gly Asp Pro Gly Glu  
 50 55 60  
 Glu Gly Lys His Gly Lys Val Gly Arg Met Gly Pro Lys Gly Ile  
 65 70 75  
 Lys Gly Glu Leu Gly Asp Met Gly Asp Gln Gly Asn Ile Gly Lys  
 80 85 90  
 Thr Gly Pro Ile Gly Lys Lys Gly Asp Lys Gly Glu Lys Gly Leu  
 95 100 105  
 Leu Gly Ile Pro Gly Glu Lys Gly Lys Ala Gly Thr Val Cys Asp  
 110 115 120  
 Cys Gly Arg Tyr Arg Lys Phe Val Gly Gln Leu Asp Ile Ser Ile  
 125 130 135  
 Ala Arg Leu Lys Thr Ser Met Lys Phe Val Lys Asn Val Ile Ala  
 140 145 150  
 Gly Ile Arg Glu Thr Glu Glu Lys Phe Tyr Tyr Ile Val Gln Glu  
 155 160 165  
 Glu Lys Asn Tyr Arg Glu Ser Leu Thr His Cys Arg Ile Arg Gly  
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 Gly Met Leu Ala Met Pro Lys Asp Glu Ala Ala Asn Thr Leu Ile  
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 Ala Asp Tyr Val Ala Lys Ser Gly Phe Phe Arg Val Phe Ile Gly

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				215					220					225					
Thr	Pro	Leu	Gln	Asn	Tyr	Ser	Asn	Trp	Asn	Glu	Gly	Glu	Pro	Ser					
				230					235					240					
Asp	Pro	Tyr	Gly	His	Glu	Asp	Cys	Val	Glu	Met	Leu	Ser	Ser	Gly					
				245					250					255					
Arg	Trp	Asn	Asp	Thr	Glu	Cys	His	Leu	Thr	Met	Tyr	Phe	Val	Cys					
				260					265					270					
Glu	Phe	Ile	Lys	Lys	Lys	Lys													
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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 98

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<210> 99

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 99

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<211> 50

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 100

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<210> 101

<211> 2574

<212> DNA

<213> Homo sapiens

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<210> 102

<211> 730

<212> PRT

<213> Homo sapiens

<400> 102

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				20					25					30

Met	Phe	Ala	Ser	Gly	Trp	Asn	Gln	Thr	Val	Pro	Ile	Glu	Glu	Ala	35	40	45
Gly	Ser	Met	Ala	Ala	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Leu	50	55	60
Pro	Leu	Leu	Leu	Leu	Lys	Leu	His	Leu	Trp	Pro	Gln	Leu	Arg	Trp	65	70	75
Leu	Pro	Ala	Asp	Leu	Ala	Phe	Ala	Val	Arg	Ala	Leu	Cys	Cys	Lys	80	85	90
Arg	Ala	Leu	Arg	Ala	Arg	Ala	Leu	Ala	Ala	Ala	Ala	Asp	Pro		95	100	105
Glu	Gly	Pro	Glu	Gly	Gly	Cys	Ser	Leu	Ala	Trp	Arg	Leu	Ala	Glu	110	115	120
Leu	Ala	Gln	Gln	Arg	Ala	Ala	His	Thr	Phe	Leu	Ile	His	Gly	Ser	125	130	135
Arg	Arg	Phe	Ser	Tyr	Ser	Glu	Ala	Glu	Arg	Glu	Ser	Asn	Arg	Ala	140	145	150
Ala	Arg	Ala	Phe	Leu	Arg	Ala	Leu	Gly	Trp	Asp	Trp	Gly	Pro	Asp	155	160	165
Gly	Gly	Asp	Ser	Gly	Glu	Gly	Ser	Ala	Gly	Glu	Gly	Glu	Arg	Ala	170	175	180
Ala	Pro	Gly	Ala	Gly	Asp	Ala	Ala	Ala	Gly	Ser	Gly	Ala	Glu	Phe	185	190	195
Ala	Gly	Gly	Asp	Gly	Ala	Ala	Arg	Gly	Gly	Gly	Ala	Ala	Ala	Pro	200	205	210
Leu	Ser	Pro	Gly	Ala	Thr	Val	Ala	Leu	Leu	Leu	Pro	Ala	Gly	Pro	215	220	225
Glu	Phe	Leu	Trp	Leu	Trp	Phe	Gly	Leu	Ala	Lys	Ala	Gly	Leu	Arg	230	235	240
Thr	Ala	Phe	Val	Pro	Thr	Ala	Leu	Arg	Arg	Gly	Pro	Leu	Leu	His	245	250	255
Cys	Leu	Arg	Ser	Cys	Gly	Ala	Arg	Ala	Leu	Val	Leu	Ala	Pro	Glu	260	265	270
Phe	Leu	Glu	Ser	Leu	Glu	Pro	Asp	Leu	Pro	Ala	Leu	Arg	Ala	Met	275	280	285
Gly	Leu	His	Leu	Trp	Ala	Ala	Gly	Pro	Gly	Thr	His	Pro	Ala	Gly	290	295	300
Ile	Ser	Asp	Leu	Leu	Ala	Glu	Val	Ser	Ala	Glu	Val	Asp	Gly	Pro	305	310	315

Val	Pro	Gly	Tyr	Leu	Ser	Ser	Pro	Gln	Ser	Ile	Thr	Asp	Thr	Cys	320	325	330
Leu	Tyr	Ile	Phe	Thr	Ser	Gly	Thr	Thr	Gly	Leu	Pro	Lys	Ala	Ala	335	340	345
Arg	Ile	Ser	His	Leu	Lys	Ile	Leu	Gln	Cys	Gln	Gly	Phe	Tyr	Gln	350	355	360
Leu	Cys	Gly	Val	His	Gln	Glu	Asp	Val	Ile	Tyr	Leu	Ala	Leu	Pro	365	370	375
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Gly	Ile	Gly	Ala	Thr	Val	Val	Leu	Lys	Ser	Lys	Phe	Ser	Ala	Gly	395	400	405
Gln	Phe	Trp	Glu	Asp	Cys	Gln	Gln	His	Arg	Val	Thr	Val	Phe	Gln	410	415	420
Tyr	Ile	Gly	Glu	Leu	Cys	Arg	Tyr	Leu	Val	Asn	Gln	Pro	Pro	Ser	425	430	435
Lys	Ala	Glu	Arg	Gly	His	Lys	Val	Arg	Leu	Ala	Val	Gly	Ser	Gly	440	445	450
Leu	Arg	Pro	Asp	Thr	Trp	Glu	Arg	Phe	Val	Arg	Arg	Phe	Gly	Pro	455	460	465
Leu	Gln	Val	Leu	Glu	Thr	Tyr	Gly	Leu	Thr	Glu	Gly	Asn	Val	Ala	470	475	480
Thr	Ile	Asn	Tyr	Thr	Gly	Gln	Arg	Gly	Ala	Val	Gly	Arg	Ala	Ser	485	490	495
Trp	Leu	Tyr	Lys	His	Ile	Phe	Pro	Phe	Ser	Leu	Ile	Arg	Tyr	Asp	500	505	510
Val	Thr	Thr	Gly	Glu	Pro	Ile	Arg	Asp	Pro	Gln	Gly	His	Cys	Met	515	520	525
Ala	Thr	Ser	Pro	Gly	Glu	Pro	Gly	Leu	Leu	Val	Ala	Pro	Val	Ser	530	535	540
Gln	Gln	Ser	Pro	Phe	Leu	Gly	Tyr	Ala	Gly	Gly	Pro	Glu	Leu	Ala	545	550	555
Gln	Gly	Lys	Leu	Leu	Lys	Asp	Val	Phe	Arg	Pro	Gly	Asp	Val	Phe	560	565	570
Phe	Asn	Thr	Gly	Asp	Leu	Leu	Val	Cys	Asp	Asp	Gln	Gly	Phe	Leu	575	580	585
Arg	Phe	His	Asp	Arg	Thr	Gly	Asp	Thr	Phe	Arg	Trp	Lys	Gly	Glu	590	595	600

Asn	Val	Ala	Thr	Thr	Glu	Val	Ala	Glu	Val	Phe	Glu	Ala	Leu	Asp	
				605					610					615	
Phe	Leu	Gln	Glu	Val	Asn	Val	Tyr	Gly	Val	Thr	Val	Pro	Gly	His	
				620					625					630	
Glu	Gly	Arg	Ala	Gly	Met	Ala	Ala	Leu	Val	Leu	Arg	Pro	Pro	His	
				635					640					645	
Ala	Leu	Asp	Leu	Met	Gln	Leu	Tyr	Thr	His	Val	Ser	Glu	Asn	Leu	
				650					655					660	
Pro	Pro	Tyr	Ala	Arg	Pro	Arg	Phe	Leu	Arg	Leu	Gln	Glu	Ser	Leu	
				665					670					675	
Ala	Thr	Thr	Glu	Thr	Phe	Lys	Gln	Gln	Lys	Val	Arg	Met	Ala	Asn	
				680					685					690	
Glu	Gly	Phe	Asp	Pro	Ser	Thr	Leu	Ser	Asp	Pro	Leu	Tyr	Val	Leu	
				695					700					705	
Asp	Gln	Ala	Val	Gly	Ala	Tyr	Leu	Pro	Leu	Thr	Thr	Ala	Arg	Tyr	
				710					715					720	
Ser	Ala	Leu	Leu	Ala	Gly	Asn	Leu	Arg	Ile						
				725					730						

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 <212> DNA  
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<220>  
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<400> 103  
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<210> 104  
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 <213> Artificial Sequence

<220>  
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<400> 104  
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<210> 105  
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 <212> DNA  
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<220>  
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<400> 105  
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<210> 106  
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<212> DNA  
<213> Artificial Sequence

<220>  
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<400> 106  
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<210> 107  
<211> 45  
<212> DNA  
<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<210> 108  
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<213> Homo sapiens

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acgcgcgcat acacactcgc tctcgtttgt ccattctcct cccgggggag 150  
ccggcgcgcg ctcccacctt tgccgcacac tccggcgagc cgagcccgca 200  
gcgctccagg attctgcggc tcggaactcg gattgcagct ctgaaccccc 250  
atggtggttt tttaaact tcttttcctt ctcttcctcg ttttgattgc 300  
accgtttcca tctgggggct agaggagcaa ggcagcagcc ttcccagcca 350  
gcccttggtg gcttgccatc gtccatctgg cttataaaag tttgctgagc 400  
gcagtccaga gggctgcgct gctcgtcccc tcggctggca gaagggggtg 450  
acgctgggca gcggcgagga gcgcgccgct gcctctggcg ggctttcggc 500  
ttgaggggca aggtgaagag cgcaccggcc gtgggggtta ccgagctgga 550  
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 gatgaaactg catttttagct atctgaatgg ccaactcact tcttttctta 2300  
 cactcttggg caatggacca tgccacaaaa acttaccgtt ttctatgaga 2350  
 agagagcagt aatgcaatct gcctcccttt ttgttttccc aaagagtacc 2400  
 ggggtgccaga ctgaactgct tcctctttcc ttcagctatc tgtggggacc 2450  
 ttgtttattc tagagagaat tcttactcaa atttttcgta ccaggagatt 2500  
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 gtgaggggttt tttttttctc atttaaaat 2579

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 <211> 555  
 <212> PRT  
 <213> Homo sapiens

<400> 109  
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 Gly Glu Val Arg Gln Ala Tyr Gly Ala Lys Gly Phe Ser Leu Ala  
 35 40 45  
 Asp Ile Pro Tyr Gln Glu Ile Ala Gly Glu His Leu Arg Ile Cys  
 50 55 60  
 Pro Gln Glu Tyr Thr Cys Cys Thr Thr Glu Met Glu Asp Lys Leu  
 65 70 75  
 Ser Gln Gln Ser Lys Leu Glu Phe Glu Asn Leu Val Glu Glu Thr  
 80 85 90  
 Ser His Phe Val Arg Thr Thr Phe Val Ser Arg His Lys Lys Phe  
 95 100 105  
 Asp Glu Phe Phe Arg Glu Leu Leu Glu Asn Ala Glu Lys Ser Leu  
 110 115 120  
 Asn Asp Met Phe Val Arg Thr Tyr Gly Met Leu Tyr Met Gln Asn  
 125 130 135  
 Ser Glu Val Phe Gln Asp Leu Phe Thr Glu Leu Lys Arg Tyr Tyr  
 140 145 150

Thr	Gly	Gly	Asn	Val	Asn	Leu	Glu	Glu	Met	Leu	Asn	Asp	Phe	Trp	155	160	165
Ala	Arg	Leu	Leu	Glu	Arg	Met	Phe	Gln	Leu	Ile	Asn	Pro	Gln	Tyr	170	175	180
His	Phe	Ser	Glu	Asp	Tyr	Leu	Glu	Cys	Val	Ser	Lys	Tyr	Thr	Asp	185	190	195
Gln	Leu	Lys	Pro	Phe	Gly	Asp	Val	Pro	Arg	Lys	Leu	Lys	Ile	Gln	200	205	210
Val	Thr	Arg	Ala	Phe	Ile	Ala	Ala	Arg	Thr	Phe	Val	Gln	Gly	Leu	215	220	225
Thr	Val	Gly	Arg	Glu	Val	Ala	Asn	Arg	Val	Ser	Lys	Val	Ser	Pro	230	235	240
Thr	Pro	Gly	Cys	Ile	Arg	Ala	Leu	Met	Lys	Met	Leu	Tyr	Cys	Pro	245	250	255
Tyr	Cys	Arg	Gly	Leu	Pro	Thr	Val	Arg	Pro	Cys	Asn	Asn	Tyr	Cys	260	265	270
Leu	Asn	Val	Met	Lys	Gly	Cys	Leu	Ala	Asn	Gln	Ala	Asp	Leu	Asp	275	280	285
Thr	Glu	Trp	Asn	Leu	Phe	Ile	Asp	Ala	Met	Leu	Leu	Val	Ala	Glu	290	295	300
Arg	Leu	Glu	Gly	Pro	Phe	Asn	Ile	Glu	Ser	Val	Met	Asp	Pro	Ile	305	310	315
Asp	Val	Lys	Ile	Ser	Glu	Ala	Ile	Met	Asn	Met	Gln	Glu	Asn	Ser	320	325	330
Met	Gln	Val	Ser	Ala	Lys	Val	Phe	Gln	Gly	Cys	Gly	Gln	Pro	Lys	335	340	345
Pro	Ala	Pro	Ala	Leu	Arg	Ser	Ala	Arg	Ser	Ala	Pro	Glu	Asn	Phe	350	355	360
Asn	Thr	Arg	Phe	Arg	Pro	Tyr	Asn	Pro	Glu	Glu	Arg	Pro	Thr	Thr	365	370	375
Ala	Ala	Gly	Thr	Ser	Leu	Asp	Arg	Leu	Val	Thr	Asp	Ile	Lys	Glu	380	385	390
Lys	Leu	Lys	Leu	Ser	Lys	Lys	Val	Trp	Ser	Ala	Leu	Pro	Tyr	Thr	395	400	405
Ile	Cys	Lys	Asp	Glu	Ser	Val	Thr	Ala	Gly	Thr	Ser	Asn	Glu	Glu	410	415	420
Glu	Cys	Trp	Asn	Gly	His	Ser	Lys	Ala	Arg	Tyr	Leu	Pro	Glu	Ile	425	430	435

Met	Asn	Asp	Gly	Leu	Thr	Asn	Gln	Ile	Asn	Asn	Pro	Glu	Val	Asp	
				440					445					450	
Val	Asp	Ile	Thr	Arg	Pro	Asp	Thr	Phe	Ile	Arg	Gln	Gln	Ile	Met	
				455					460					465	
Ala	Leu	Arg	Val	Met	Thr	Asn	Lys	Leu	Lys	Asn	Ala	Tyr	Asn	Gly	
				470					475					480	
Asn	Asp	Val	Asn	Phe	Gln	Asp	Thr	Ser	Asp	Glu	Ser	Ser	Gly	Ser	
				485					490					495	
Gly	Ser	Gly	Ser	Gly	Cys	Met	Asp	Asp	Val	Cys	Pro	Thr	Glu	Phe	
				500					505					510	
Glu	Phe	Val	Thr	Thr	Glu	Ala	Pro	Ala	Val	Asp	Pro	Asp	Arg	Arg	
				515					520					525	
Glu	Val	Asp	Ser	Ser	Ala	Ala	Gln	Arg	Gly	His	Ser	Leu	Leu	Ser	
				530					535					540	
Trp	Ser	Leu	Thr	Cys	Ile	Val	Leu	Ala	Leu	Gln	Arg	Leu	Cys	Arg	
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<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 110

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<210> 111

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 111

tgacacgtct ctgcagtgcc cagg 24

<210> 112

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 112

gaatgctgga acgggcacag caaagccaga tacttgctg 40

<210> 113  
<211> 4649  
<212> DNA  
<213> Homo sapiens

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cgccaactac gcaaagacca agcgggctcc gcgcggaccg gccgcggggc 150  
tagggacccg gctttggcct tcaggctccc tagcagcggg gaaaaggaat 200  
tgctgcccg agtttctgcg gaggtggagg gagatcagga aacggcttct 250  
tcctcacttc gccgcctggt gagtgtcggg gagattggca aacgcctagg 300  
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 <211> 515  
 <212> PRT  
 <213> Homo. sapiens

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 35 40 45  
 Trp Gly Gln Ala Leu Glu Glu Glu Glu Gly Ala Leu Leu Ala  
 50 55 60  
 Gln Ala Gly Glu Lys Leu Glu Pro Ser Thr Thr Ser Thr Ser Gln  
 65 70 75  
 Pro His Leu Ile Phe Ile Leu Ala Asp Asp Gln Gly Phe Arg Asp  
 80 85 90  
 Val Gly Tyr His Gly Ser Glu Ile Lys Thr Pro Thr Leu Asp Lys  
 95 100 105  
 Leu Ala Ala Glu Gly Val Lys Leu Glu Asn Tyr Tyr Val Gln Pro  
 110 115 120  
 Ile Cys Thr Pro Ser Arg Ser Gln Phe Ile Thr Gly Lys Tyr Gln  
 125 130 135  
 Ile His Thr Gly Leu Gln His Ser Ile Ile Arg Pro Thr Gln Pro  
 140 145 150

Asn Cys Leu Pro	Leu Asp Asn Ala Thr	Leu Pro Gln Lys Leu	Lys
155	160		165
Glu Val Gly Tyr	Ser Thr His Met Val	Gly Lys Trp His Leu	Gly
170	175		180
Phe Asn Arg Lys	Glu Cys Met Pro Thr	Arg Arg Gly Phe Asp	Thr
185	190		195
Phe Phe Gly Ser	Leu Leu Gly Ser Gly	Asp Tyr Tyr Thr His	Tyr
200	205		210
Lys Cys Asp Ser	Pro Gly Met Cys Gly	Tyr Asp Leu Tyr Glu	Asn
215	220		225
Asp Asn Ala Ala	Trp Asp Tyr Asp Asn	Gly Ile Tyr Ser Thr	Gln
230	235		240
Met Tyr Thr Gln	Arg Val Gln Gln Ile	Leu Ala Ser His Asn	Pro
245	250		255
Thr Lys Pro Ile	Phe Leu Tyr Thr Ala	Tyr Gln Ala Val His	Ser
260	265		270
Pro Leu Gln Ala	Pro Gly Arg Tyr Phe	Glu His Tyr Arg Ser	Ile
275	280		285
Ile Asn Ile Asn	Arg Arg Arg Tyr Ala	Ala Met Leu Ser Cys	Leu
290	295		300
Asp Glu Ala Ile	Asn Asn Val Thr Leu	Ala Leu Lys Thr Tyr	Gly
305	310		315
Phe Tyr Asn Asn	Ser Ile Ile Ile Tyr	Ser Ser Asp Asn Gly	Gly
320	325		330
Gln Pro Thr Ala	Gly Gly Ser Asn Trp	Pro Leu Arg Gly Ser	Lys
335	340		345
Gly Thr Tyr Trp	Glu Gly Gly Ile Arg	Ala Val Gly Phe Val	His
350	355		360
Ser Pro Leu Leu	Lys Asn Lys Gly Thr	Val Cys Lys Glu Leu	Val
365	370		375
His Ile Thr Asp	Trp Tyr Pro Thr Leu	Ile Ser Leu Ala Glu	Gly
380	385		390
Gln Ile Asp Glu	Asp Ile Gln Leu Asp	Gly Tyr Asp Ile Trp	Glu
395	400		405
Thr Ile Ser Glu	Gly Leu Arg Ser Pro	Arg Val Asp Ile Leu	His
410	415		420
Asn Ile Asp Pro	Tyr Thr Pro Arg Gln	Lys Met Ala Pro Gly	Gln
425	430		435

Gln	Ala	Met	Gly	Ser	Gly	Thr	Leu	Gln	Ser	Ser	Gln	Pro	Ser	Glu
				440					445					450
Cys	Ser	Thr	Gly	Asn	Cys	Leu	Gln	Glu	Ile	Leu	Ala	Thr	Ala	Thr
				455					460					465
Gly	Ser	Pro	Leu	Ser	Leu	Ser	Ala	Thr	Trp	Asp	Arg	Thr	Gly	Gly
				470					475					480
Thr	Met	Asn	Gly	Ser	Pro	Cys	Gln	Leu	Ala	Lys	Val	Tyr	Gly	Phe
				485					490					495
Ser	Thr	Ser	Gln	Pro	Thr	His	Met	Arg	Gly	Trp	Thr	Tyr	Leu	Thr
				500					505					510
Gly	Ile	Gln	Glu	Ser										
				515										

<210> 115  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 115  
 cccaacccaa ctgtttacct ctgg 24

<210> 116  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 116  
 ctctctgagt gtacatctgt gtgg 24

<210> 117  
 <211> 53  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<220>  
 <221> unsure  
 <222> 33  
 <223> unknown base

<400> 117  
 gccaccctac ctcagaaact gaaggaggtt ggntattcaa cgcatatggt 50

cgg 53

<210> 118

<211> 2260

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 2009, 2026, 2033, 2055, 2074, 2078, 2086

<223> unknown base

<400> 118

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ggaggcggcg gcttagctgc tacggggtcc ggccggcgcc ctcccgaggg 100  
gggctcagga ggaggaagga ggacccgtgc gagaatgcct ctgccctgga 150  
gccttgcgct cccgctgctg ctctcctggg tggcaggtgg ttccgggaac 200  
gcggccagtg caaggcatca cgggttggtta gcatcggcac gtcagcctgg 250  
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acagcaaggg agtctgtgaa gctacatgcg aacctggatg taagtttggt 350  
gagtgcgtgg gaccaaacia atgcagatgc ttccaggat acaccgggaa 400  
aacctgcagt caagatgtga atgagtgtgg aatgaaaccc cggccatgcc 450  
aacacagatg tgtgaataca cacggaagct acaagtgctt ttgcctcagt 500  
ggccacatgc tcatgccaga tgctacgtgt gtgaactcta ggacatgtgc 550  
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aagatgtgtg aacacatttg gaagctacta ctgcaaattg cacattgggt 750  
tcgaactgca atatatcagt ggacgatatg actgtataga tataaatgaa 800  
tgtactatgg atagccatac gtgcagccac catgccatt gcttcaatac 850  
ccaagggtcc ttcaagtgtg aatgcaagca gggatataaa ggcaatggac 900  
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cctggtacca tcaaagacag aatcaagaag ttgcttgctc aaaaaaacag 1000  
catgaaaaag aaggcaaaaa ttaaaaatgt taccacagaa cccaccagga 1050  
ctcctacccc taaggtgaac ttgcagccct tcaactatga agagatagtt 1100

tccagaggcg ggaactctca tggaggtaaa aaaggggaatg aagagaaatg 1150  
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 catagaggag cgaagcctgc gaggagatgt gtttttcctt aaggtgaatg 1250  
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 ctgctgatcg agataatgct attggcttct atatggcagt tccggccttg 1450  
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 aacgtggcaa gggcaaaacc ggcgaaatcg cagtggatgg cgtcttgctt 1750  
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 actatcttta tatttgactt tgtatgtcag ttccctgggt tttttgatat 1850  
 tgcacatag gacctctggc attttagaat tactagctga aaaattgtaa 1900  
 tgtaccaaca gaaatattat tgtaagatgc ctttcttgta taagatatgc 1950  
 caatatattgc tttaaatatt atatcactgt atcttctcag tcattttctga 2000  
 atcttttcnc attatattat aaaatntgga aangtcagtt tatctcccct 2050  
 cctngtata tctgatttgt atangtangt tgatgngctt ctctctacaa 2100  
 catttctaga aaatagaaaa aaaagcacag agaaatgttt aactgtttga 2150  
 ctcttatgat acttcttgga aactatgaca tcaaagatag acttttgcct 2200  
 aagtggctta gctgggtctt tcatagccaa acttgtatat ttaattcttt 2250  
 gtaataataa 2260

<210> 119

<211> 338

<212> PRT

<213> Homo sapiens

<400> 119

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Val	Ala	Gly	Gly	Phe	Gly	Asn	Ala	Ala	Ser	Ala	Arg	His	His	Gly	
				20					25					30	
Leu	Leu	Ala	Ser	Ala	Arg	Gln	Pro	Gly	Val	Cys	His	Tyr	Gly	Thr	
				35					40					45	
Lys	Leu	Ala	Cys	Cys	Tyr	Gly	Trp	Arg	Arg	Asn	Ser	Lys	Gly	Val	
				50					55					60	
Cys	Glu	Ala	Thr	Cys	Glu	Pro	Gly	Cys	Lys	Phe	Gly	Glu	Cys	Val	
				65					70					75	
Gly	Pro	Asn	Lys	Cys	Arg	Cys	Phe	Pro	Gly	Tyr	Thr	Gly	Lys	Thr	
				80					85					90	
Cys	Ser	Gln	Asp	Val	Asn	Glu	Cys	Gly	Met	Lys	Pro	Arg	Pro	Cys	
				95					100					105	
Gln	His	Arg	Cys	Val	Asn	Thr	His	Gly	Ser	Tyr	Lys	Cys	Phe	Cys	
				110					115					120	
Leu	Ser	Gly	His	Met	Leu	Met	Pro	Asp	Ala	Thr	Cys	Val	Asn	Ser	
				125					130					135	
Arg	Thr	Cys	Ala	Met	Ile	Asn	Cys	Gln	Tyr	Ser	Cys	Glu	Asp	Thr	
				140					145					150	
Glu	Glu	Gly	Pro	Gln	Cys	Leu	Cys	Pro	Ser	Ser	Gly	Leu	Arg	Leu	
				155					160					165	
Ala	Pro	Asn	Gly	Arg	Asp	Cys	Leu	Asp	Ile	Asp	Glu	Cys	Ala	Ser	
				170					175					180	
Gly	Lys	Val	Ile	Cys	Pro	Tyr	Asn	Arg	Arg	Cys	Val	Asn	Thr	Phe	
				185					190					195	
Gly	Ser	Tyr	Tyr	Cys	Lys	Cys	His	Ile	Gly	Phe	Glu	Leu	Gln	Tyr	
				200					205					210	
Ile	Ser	Gly	Arg	Tyr	Asp	Cys	Ile	Asp	Ile	Asn	Glu	Cys	Thr	Met	
				215					220					225	
Asp	Ser	His	Thr	Cys	Ser	His	His	Ala	Asn	Cys	Phe	Asn	Thr	Gln	
				230					235					240	
Gly	Ser	Phe	Lys	Cys	Lys	Cys	Lys	Gln	Gly	Tyr	Lys	Gly	Asn	Gly	
				245					250					255	
Leu	Arg	Cys	Ser	Ala	Ile	Pro	Glu	Asn	Ser	Val	Lys	Glu	Val	Leu	
				260					265					270	
Arg	Ala	Pro	Gly	Thr	Ile	Lys	Asp	Arg	Ile	Lys	Lys	Leu	Leu	Ala	
				275					280					285	
His	Lys	Asn	Ser	Met	Lys	Lys	Lys	Ala	Lys	Ile	Lys	Asn	Val	Thr	
				290					295					300	

Pro	Glu	Pro	Thr	Arg	Thr	Pro	Thr	Pro	Lys	Val	Asn	Leu	Gln	Pro
				305					310					315
Phe	Asn	Tyr	Glu	Glu	Ile	Val	Ser	Arg	Gly	Gly	Asn	Ser	His	Gly
				320					325					330
Gly	Lys	Lys	Gly	Asn	Glu	Glu	Lys							
				335										

<210> 120  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 120  
 cctcagtggc cacatgctca tg 22

<210> 121  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 121  
 ggctgcacgt atggctatcc atag 24

<210> 122  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 122  
 gataaactgt cagtacagct gtgaagacac agaagaaggg ccacagtgcc 50

<210> 123  
 <211> 1199  
 <212> DNA  
 <213> Homo sapiens

<400> 123  
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 gtgcagctgc tgcgcttctt gagggctgac ggcgacctga cgctactatg 100  
 ggccgagtgg cagggacgac gcccagaatg ggagctgact gatatgggtg 150  
 tgtgggtgac tggagcctcg agtgggaattg gtgaggagct ggcttaccag 200  
 ttgtctaaac taggagtttc tcttgtgctg tcagccagaa gagtgcata 250

gctggaaagg gtgaaaagaa gatgcctaga gaatggcaat ttaaaagaaa 300  
aagatatact tgttttgccc cttgacctga ccgacctgg ttcccatgaa 350  
gcggctacca aagctgttct ccaggagttt ggtagaatcg acattctggt 400  
caacaatggt ggaatgtccc agcgttctct gtgcatggat accagcttgg 450  
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acaaaatgtg ttctgcctca catgatcgag aggaagcaag gaaagattgt 550  
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gaacttgcca cataccagg tataatagtt tctaacattt gcccaggacc 700  
tgtgcaatca aatattgtgg agaattccct agctggagaa gtcacaaaga 750  
ctataggcaa taatggagac cagtcccaca agatgacaac cagtcgttgt 800  
gtgcggctga tgttaatcag catggccaat gatttgaaag aagtttggat 850  
ctcagaacaa cttttcttgt tagtaacata tttgtggcaa tacatgcaa 900  
cctgggcctg gtggataacc aacaagatgg ggaagaaaag gattgagaac 950  
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aaaacatgac tgaaaagagc acctgtactt ttcaagccac tggagggaga 1050  
aatggaaaac atgaaaacag caatcttctt atgcttctga ataatcaaag 1100  
actaatttgt gattttactt tttaatagat atgactttgc ttccaacatg 1150  
gaatgaaata aaaaataaat aataaaagat tgccatgaat cttgcaaaa 1199

<210> 124  
<211> 289  
<212> PRT  
<213> Homo sapiens

<400> 124  
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1 5 10 15  
Leu Ala Tyr Gln Leu Ser Lys Leu Gly Val Ser Leu Val Leu Ser  
20 25 30  
Ala Arg Arg Val His Glu Leu Glu Arg Val Lys Arg Arg Cys Leu  
35 40 45  
Glu Asn Gly Asn Leu Lys Glu Lys Asp Ile Leu Val Leu Pro Leu  
50 55 60



Asp	Leu	Thr	Asp	Thr	Gly	Ser	His	Glu	Ala	Ala	Thr	Lys	Ala	Val	
				65					70					75	
Leu	Gln	Glu	Phe	Gly	Arg	Ile	Asp	Ile	Leu	Val	Asn	Asn	Gly	Gly	
				80					85					90	
Met	Ser	Gln	Arg	Ser	Leu	Cys	Met	Asp	Thr	Ser	Leu	Asp	Val	Tyr	
				95					100					105	
Arg	Lys	Leu	Ile	Glu	Leu	Asn	Tyr	Leu	Gly	Thr	Val	Ser	Leu	Thr	
				110					115					120	
Lys	Cys	Val	Leu	Pro	His	Met	Ile	Glu	Arg	Lys	Gln	Gly	Lys	Ile	
				125					130					135	
Val	Thr	Val	Asn	Ser	Ile	Leu	Gly	Ile	Ile	Ser	Val	Pro	Leu	Ser	
				140					145					150	
Ile	Gly	Tyr	Cys	Ala	Ser	Lys	His	Ala	Leu	Arg	Gly	Phe	Phe	Asn	
				155					160					165	
Gly	Leu	Arg	Thr	Glu	Leu	Ala	Thr	Tyr	Pro	Gly	Ile	Ile	Val	Ser	
				170					175					180	
Asn	Ile	Cys	Pro	Gly	Pro	Val	Gln	Ser	Asn	Ile	Val	Glu	Asn	Ser	
				185					190					195	
Leu	Ala	Gly	Glu	Val	Thr	Lys	Thr	Ile	Gly	Asn	Asn	Gly	Asp	Gln	
				200					205					210	
Ser	His	Lys	Met	Thr	Thr	Ser	Arg	Cys	Val	Arg	Leu	Met	Leu	Ile	
				215					220					225	
Ser	Met	Ala	Asn	Asp	Leu	Lys	Glu	Val	Trp	Ile	Ser	Glu	Gln	Pro	
				230					235					240	
Phe	Leu	Leu	Val	Thr	Tyr	Leu	Trp	Gln	Tyr	Met	Pro	Thr	Trp	Ala	
				245					250					255	
Trp	Trp	Ile	Thr	Asn	Lys	Met	Gly	Lys	Lys	Arg	Ile	Glu	Asn	Phe	
				260					265					270	
Lys	Ser	Gly	Val	Asp	Ala	Asp	Ser	Ser	Tyr	Phe	Lys	Ile	Phe	Lys	
				275					280					285	

Thr Lys His Asp

<210> 125

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 125

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<210> 126

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 126

ctgtgaatag catcctggg 19

<210> 127

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 127

cttttcaagc cactggaggg 20

<210> 128

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 128

ctgtagacat ccaagctggt atcc 24

<210> 129

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 129

aagagtctgc atccacacca etc 23

<210> 130

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 130

acctgacgct actatgggcc gagtggcagg gacgacgccc agaag 46

<210> 131  
<211> 2365  
<212> DNA  
<213> Homo sapiens

<400> 131  
gcgacgtggg caccgccatc agctgttcgc gcgtcttctc ctccaggtgg 50  
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caatcaatcc aacagcatat tcggttgcat cttctacaca ctacagctat 150  
tgttaggttg cctgcggaca cgctgggcct ctgtcctgat gctgctgagc 200  
tccctgggtgt ctctcgctgg ttctgtctac ctggcctgga tcctgttctt 250  
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 cttgccaagg ccccgccagg ccggcgtct tcaccgcgt ccctgcctat 1900  
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 cctcctttac tctttcagat acaatcacgc cagccacgtt gttttgaaaa 2300  
 tttctttttt tggggggcag cagttttcct ttttttaaac ttaaataaat 2350  
 tgttacaaaa taaaa 2365

<210> 132

<211> 571

<212> PRT

<213> Homo sapiens

<400> 132

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Ala	Trp	Ile	Leu	Phe	Phe	Val	Leu	Tyr	Asp	Phe	Cys	Ile	Val	Cys
				20					25					30

Ile	Thr	Thr	Tyr	Ala	Ile	Asn	Val	Ser	Leu	Met	Trp	Leu	Ser	Phe	35	40	45
Arg	Lys	Val	Gln	Glu	Pro	Gln	Gly	Lys	Ala	Lys	Arg	His	Gly	Asn	50	55	60
Thr	Val	Pro	Gly	Glu	Trp	Pro	Trp	Gln	Ala	Ser	Val	Arg	Arg	Gln	65	70	75
Gly	Ala	His	Ile	Cys	Ser	Gly	Ser	Leu	Val	Ala	Asp	Thr	Trp	Val	80	85	90
Leu	Thr	Ala	Ala	His	Cys	Phe	Glu	Lys	Ala	Ala	Ala	Thr	Glu	Leu	95	100	105
Asn	Ser	Trp	Ser	Val	Val	Leu	Gly	Ser	Leu	Gln	Arg	Glu	Gly	Leu	110	115	120
Ser	Pro	Gly	Ala	Glu	Glu	Val	Gly	Val	Ala	Ala	Leu	Gln	Leu	Pro	125	130	135
Arg	Ala	Tyr	Asn	His	Tyr	Ser	Gln	Gly	Ser	Asp	Leu	Ala	Leu	Leu	140	145	150
Gln	Leu	Ala	His	Pro	Thr	Thr	His	Thr	Pro	Leu	Cys	Leu	Pro	Gln	155	160	165
Pro	Ala	His	Arg	Phe	Pro	Phe	Gly	Ala	Ser	Cys	Trp	Ala	Thr	Gly	170	175	180
Trp	Asp	Gln	Asp	Thr	Ser	Asp	Ala	Pro	Gly	Thr	Leu	Arg	Asn	Leu	185	190	195
Arg	Leu	Arg	Leu	Ile	Ser	Arg	Pro	Thr	Cys	Asn	Cys	Ile	Tyr	Asn	200	205	210
Gln	Leu	His	Gln	Arg	His	Leu	Ser	Asn	Pro	Ala	Arg	Pro	Gly	Met	215	220	225
Leu	Cys	Gly	Gly	Pro	Gln	Pro	Gly	Val	Gln	Gly	Pro	Cys	Gln	Gly	230	235	240
Asp	Ser	Gly	Gly	Pro	Val	Leu	Cys	Leu	Glu	Pro	Asp	Gly	His	Trp	245	250	255
Val	Gln	Ala	Gly	Ile	Ile	Ser	Phe	Ala	Ser	Ser	Cys	Ala	Gln	Glu	260	265	270
Asp	Ala	Pro	Val	Leu	Leu	Thr	Asn	Thr	Ala	Ala	His	Ser	Ser	Trp	275	280	285
Leu	Gln	Ala	Arg	Val	Gln	Gly	Ala	Ala	Phe	Leu	Ala	Gln	Ser	Pro	290	295	300
Glu	Thr	Pro	Glu	Met	Ser	Asp	Glu	Asp	Ser	Cys	Val	Ala	Cys	Gly	305	310	315

Ser	Leu	Arg	Thr	Ala	Gly	Pro	Gln	Ala	Gly	Ala	Pro	Ser	Pro	Trp
				320					325					330
Pro	Trp	Glu	Ala	Arg	Leu	Met	His	Gln	Gly	Gln	Leu	Ala	Cys	Gly
				335					340					345
Gly	Ala	Leu	Val	Ser	Glu	Glu	Ala	Val	Leu	Thr	Ala	Ala	His	Cys
				350					355					360
Phe	Ile	Gly	Arg	Gln	Ala	Pro	Glu	Glu	Trp	Ser	Val	Gly	Leu	Gly
				365					370					375
Thr	Arg	Pro	Glu	Glu	Trp	Gly	Leu	Lys	Gln	Leu	Ile	Leu	His	Gly
				380					385					390
Ala	Tyr	Thr	His	Pro	Glu	Gly	Gly	Tyr	Asp	Met	Ala	Leu	Leu	Leu
				395					400					405
Leu	Ala	Gln	Pro	Val	Thr	Leu	Gly	Ala	Ser	Leu	Arg	Pro	Leu	Cys
				410					415					420
Leu	Pro	Tyr	Pro	Asp	His	His	Leu	Pro	Asp	Gly	Glu	Arg	Gly	Trp
				425					430					435
Val	Leu	Gly	Arg	Ala	Arg	Pro	Gly	Ala	Gly	Ile	Ser	Ser	Leu	Gln
				440					445					450
Thr	Val	Pro	Val	Thr	Leu	Leu	Gly	Pro	Arg	Ala	Cys	Ser	Arg	Leu
				455					460					465
His	Ala	Ala	Pro	Gly	Gly	Asp	Gly	Ser	Pro	Ile	Leu	Pro	Gly	Met
				470					475					480
Val	Cys	Thr	Ser	Ala	Val	Gly	Glu	Leu	Pro	Ser	Cys	Glu	Gly	Leu
				485					490					495
Ser	Gly	Ala	Pro	Leu	Val	His	Glu	Val	Arg	Gly	Thr	Trp	Phe	Leu
				500					505					510
Ala	Gly	Leu	His	Ser	Phe	Gly	Asp	Ala	Cys	Gln	Gly	Pro	Ala	Arg
				515					520					525
Pro	Ala	Val	Phe	Thr	Ala	Leu	Pro	Ala	Tyr	Glu	Asp	Trp	Val	Ser
				530					535					540
Ser	Leu	Asp	Trp	Gln	Val	Tyr	Phe	Ala	Glu	Glu	Pro	Glu	Pro	Glu
				545					550					555
Ala	Glu	Pro	Gly	Ser	Cys	Leu	Ala	Asn	Ile	Ser	Gln	Pro	Thr	Ser
				560					565					570

Cys

<210> 133

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 133

cctgtgctgt gcctcgagcc tgac 24

<210> 134

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 134

gtgggcagca gttagcaccg cctc 24

<210> 135

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 135

ggctggcatc atcagctttg catcaagctg tgcccaggag gacgc 45

<210> 136

<211> 1998

<212> DNA

<213> Homo sapiens

<400> 136

cgggccgccc ccggccccc ttcgggccgg gcctcgctgc ggcggcgact 50

gagccaggct gggccgcgtc cctgagtccc agagtcggcg cggcgcgga 100

ggggcagcct tccaccacgg ggagcccagc tgtcagccgc ctcacaggaa 150

gatgtgcgt cggcggggca gccctggcat ggggtgtcat gtgggtgcag 200

ccctgggagc actgtggttc tgcctcacag gagccctgga ggtccaggtc 250

cctgaagacc cagtgtgtgc actggtgggc accgatgcca ccctgtgctg 300

ctccttctcc cctgagcctg gcttcagcct ggcacagctc aacctcatct 350

ggcagctgac agatacaaaa cagctggtgc acagctttgc tgagggccag 400

gaccagggca ggcctatgc caaccgcacg gccctcttcc cggacctgct 450

ggcacagggc aacgcatccc tgaggctgca gcgcgtgcgt gtggcgagc 500

agggcagctt cacctgcttc gtgagcatcc gggatttcgg cagcgctgcc 550

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attttgggga aaataaatgt ctttgtaaaa aaaaaaaaaa aaaaaaaaa 1998

<210> 137

<211> 316

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

<222> 233

<223> unknown amino acid

<400> 137

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Ala	Ala	Leu	Gly	Ala	Leu	Trp	Phe	Cys	Leu	Thr	Gly	Ala	Leu	Glu
			20						25					30

Val	Gln	Val	Pro	Glu	Asp	Pro	Val	Val	Ala	Leu	Val	Gly	Thr	Asp
				35					40					45

Ala	Thr	Leu	Cys	Cys	Ser	Phe	Ser	Pro	Glu	Pro	Gly	Phe	Ser	Leu
				50					55					60

Ala	Gln	Leu	Asn	Leu	Ile	Trp	Gln	Leu	Thr	Asp	Thr	Lys	Gln	Leu
				65					70					75

Val	His	Ser	Phe	Ala	Glu	Gly	Gln	Asp	Gln	Gly	Ser	Ala	Tyr	Ala
				80					85					90

Asn	Arg	Thr	Ala	Leu	Phe	Pro	Asp	Leu	Leu	Ala	Gln	Gly	Asn	Ala
				95					100					105

Ser	Leu	Arg	Leu	Gln	Arg	Val	Arg	Val	Ala	Asp	Glu	Gly	Ser	Phe
				110					115					120

Thr	Cys	Phe	Val	Ser	Ile	Arg	Asp	Phe	Gly	Ser	Ala	Ala	Val	Ser
				125					130					135

Leu	Gln	Val	Ala	Ala	Pro	Tyr	Ser	Lys	Pro	Ser	Met	Thr	Leu	Glu
				140					145					150

Pro	Asn	Lys	Asp	Leu	Arg	Pro	Gly	Asp	Thr	Val	Thr	Ile	Thr	Cys
				155					160					165

Ser	Ser	Tyr	Gln	Gly	Tyr	Pro	Glu	Ala	Glu	Val	Phe	Trp	Gln	Asp
				170					175					180

Gly	Gln	Gly	Val	Pro	Leu	Thr	Gly	Asn	Val	Thr	Thr	Ser	Gln	Met
				185					190					195

Ala	Asn	Glu	Gln	Gly	Leu	Phe	Asp	Val	His	Ser	Val	Leu	Arg	Val
				200					205					210

Val	Leu	Gly	Ala	Asn	Gly	Thr	Tyr	Ser	Cys	Leu	Val	Arg	Asn	Pro
				215					220					225

Val	Leu	Gln	Gln	Asp	Ala	His	Xaa	Ser	Val	Thr	Ile	Thr	Gly	Gln	230	235	240
Pro	Met	Thr	Phe	Pro	Pro	Glu	Ala	Leu	Trp	Val	Thr	Val	Gly	Leu	245	250	255
Ser	Val	Cys	Leu	Ile	Ala	Leu	Leu	Val	Ala	Leu	Ala	Phe	Val	Cys	260	265	270
Trp	Arg	Lys	Ile	Lys	Gln	Ser	Cys	Glu	Glu	Glu	Asn	Ala	Gly	Ala	275	280	285
Glu	Asp	Gln	Asp	Gly	Glu	Gly	Glu	Gly	Ser	Lys	Thr	Ala	Leu	Gln	290	295	300
Pro	Leu	Lys	His	Ser	Asp	Ser	Lys	Glu	Asp	Asp	Gly	Gln	Glu	Ile	305	310	315

Ala

<210> 138

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 138

ctggcacagc tcaacctcat ctgg 24

<210> 139

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 139

gctgtctgtc tgtctcattg 20

<210> 140

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 140

ggacacagta tactgaccac 20

<210> 141

<211> 24

<212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 141  
 tgcaaccag gcagctgtaa gtgc 24  
  
 <210> 142  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 142  
 tggaagaaga gggtggtgat gtgg 24  
  
 <210> 143  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 143  
 cagctgacag acaccaaaca gctggtgcac agtttcaccg aaggc 45  
  
 <210> 144  
 <211> 2336  
 <212> DNA  
 <213> Homo sapiens  
  
 <220>  
 <221> unsure  
 <222> 1620, 1673  
 <223> unknown base  
  
 <400> 144  
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 gaagggggag tcttgaactt gtctgaagcc cttgtccgta agccttgaac 100  
 tacgttctta aatctatgaa gtcgaggac ctttcgctgc tttttagagg 150  
 acttctttcc ttgcttcagc aacatgaggc ttttcttgtg gaacgcggtc 200  
 ttgactctgt tcgtcacttc tttgattggg gctttgatcc ctgaaccaga 250  
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 aaggagggga tttgatgttg gtccactatg aaggctactt agaaaaggac 350  
 ggctccttat ttcactccac tcacaaacat aacaatggtc agcccatttg 400

gtttaccctg ggcatcctgg aggctctcaa aggttgggac cagggcttga 450  
aaggaatgtg ttaggagag aagagaaagc tcatcattcc tctgctctg 500  
ggctatggaa aagaaggaaa aggtaaaatt cccccagaaa gtacactgat 550  
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cattccaaga aatggatctt aatgatgact ggaaactctc taaagatgag 650  
gttaaagcat atttaaagaa ggagtgtgaa aaacatgggtg cgggtggtgaa 700  
tgaaagtcac catgatgctt tgggtggagga tatttttgat aaagaagatg 750  
aagacaaaga tgggtttata tctgccagag aatttacata taaacacgat 800  
gagttataga gatacatcta cccttttaat atagcactca tctttcaaga 850  
gagggcagtc atctttaaag aacattttat tttatacaa tgttctttct 900  
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 agtatattat actacaataa cattgtatca taagataaag tagtaaacca 1950  
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 tagtcccagc tactcgggag gctgagacag gagatttgct tgaacccggg 2200  
 aggcggaggt tgcagtgagc caagattgtg ccactgcact ccagcctggg 2250  
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 gcagctacta ttgaataaat acctatcctg gattttt 2336

<210> 145

<211> 211

<212> PRT

<213> Homo sapiens

<400> 145

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Ser	Leu	Ile	Gly	Ala	Leu	Ile	Pro	Glu	Pro	Glu	Val	Lys	Ile	Glu
			20					25						30
Val	Leu	Gln	Lys	Pro	Phe	Ile	Cys	His	Arg	Lys	Thr	Lys	Gly	Gly
			35					40						45
Asp	Leu	Met	Leu	Val	His	Tyr	Glu	Gly	Tyr	Leu	Glu	Lys	Asp	Gly
			50					55						60
Ser	Leu	Phe	His	Ser	Thr	His	Lys	His	Asn	Asn	Gly	Gln	Pro	Ile
			65					70						75
Trp	Phe	Thr	Leu	Gly	Ile	Leu	Glu	Ala	Leu	Lys	Gly	Trp	Asp	Gln
			80					85						90
Gly	Leu	Lys	Gly	Met	Cys	Val	Gly	Glu	Lys	Arg	Lys	Leu	Ile	Ile
			95					100						105
Pro	Pro	Ala	Leu	Gly	Tyr	Gly	Lys	Glu	Gly	Lys	Gly	Lys	Ile	Pro
			110					115						120
Pro	Glu	Ser	Thr	Leu	Ile	Phe	Asn	Ile	Asp	Leu	Leu	Glu	Ile	Arg
			125					130						135
Asn	Gly	Pro	Arg	Ser	His	Glu	Ser	Phe	Gln	Glu	Met	Asp	Leu	Asn
			140					145						150

Asp	Asp	Trp	Lys	Leu	Ser	Lys	Asp	Glu	Val	Lys	Ala	Tyr	Leu	Lys
				155					160					165
Lys	Glu	Phe	Glu	Lys	His	Gly	Ala	Val	Val	Asn	Glu	Ser	His	His
				170					175					180
Asp	Ala	Leu	Val	Glu	Asp	Ile	Phe	Asp	Lys	Glu	Asp	Glu	Asp	Lys
				185					190					195
Asp	Gly	Phe	Ile	Ser	Ala	Arg	Glu	Phe	Thr	Tyr	Lys	His	Asp	Glu
				200					205					210

Leu

<210> 146  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 146  
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<210> 147  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 147  
 gccagagca ggaggaatga tgagc 25

<210> 148  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 148  
 gtggaacgcg gtcttgactc tgttcgtcac ttctttgatt ggggctttg 49

<210> 149  
 <211> 2196  
 <212> DNA  
 <213> Homo sapiens

<400> 149  
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cagagatgcc tggctacctc gccctgcctt cagcctcacg gggctcagtc 200  
tctttttctc tttggtgcc aacaggacgga gcatggaggt cacagtacct 250  
gccaccctca acgtcctcaa tggctctgac gcccgctgc cctgcacctt 300  
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cgtgtgcctg taatcccagc tatttgggag gctgaggcag gagaatcgct 2100  
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<210> 150

<211> 215

<212> PRT

<213> Homo sapiens

<400> 150

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Gly	Leu	Ser	Leu	Phe	Phe	Ser	Leu	Val	Pro	Pro	Gly	Arg	Ser	Met
				20					25					30
Glu	Val	Thr	Val	Pro	Ala	Thr	Leu	Asn	Val	Leu	Asn	Gly	Ser	Asp
				35					40					45
Ala	Arg	Leu	Pro	Cys	Thr	Phe	Asn	Ser	Cys	Tyr	Thr	Val	Asn	His
				50					55					60
Lys	Gln	Phe	Ser	Leu	Asn	Trp	Thr	Tyr	Gln	Glu	Cys	Asn	Asn	Cys
				65					70					75
Ser	Glu	Glu	Met	Phe	Leu	Gln	Phe	Arg	Met	Lys	Ile	Ile	Asn	Leu
				80					85					90
Lys	Leu	Glu	Arg	Phe	Gln	Asp	Arg	Val	Glu	Phe	Ser	Gly	Asn	Pro
				95					100					105
Ser	Lys	Tyr	Asp	Val	Ser	Val	Met	Leu	Arg	Asn	Val	Gln	Pro	Glu



110	115	120
Asp Glu Gly Ile Tyr Asn Cys Tyr Ile	Met Asn Pro Pro Asp Arg	
125	130	135
His Arg Gly His Gly Lys Ile His Leu	Gln Val Leu Met Glu Glu	
140	145	150
Pro Pro Glu Arg Asp Ser Thr Val Ala	Val Ile Val Gly Ala Ser	
155	160	165
Val Gly Gly Phe Leu Ala Val Val Ile	Leu Val Leu Met Val Val	
170	175	180
Lys Cys Val Arg Arg Lys Lys Glu Gln	Lys Leu Ser Thr Asp Asp	
185	190	195
Leu Lys Thr Glu Glu Glu Gly Lys Thr	Asp Gly Glu Gly Asn Pro	
200	205	210
Asp Asp Gly Ala Lys		
215		

<210> 151  
 <211> 524  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 103, 233  
 <223> unknown base

<400> 151  
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 ccnactaaca tctcagtcctc tgaaaatgca cagagatgcc tggctacctc 150  
 gccctgcctt cagcctcagc gggctcagtc tctttttctc tttggtgcca 200  
 ccaggacgga gcatggaggt ccacagtacc tgnccaccct caacgtcctc 250  
 aatggctctg acgcccgcct gccctgccct tcaactcctg ctacacagtg 300  
 aaccacaaac agttctccct gaactggact taccaggagt gcaacaactg 350  
 ctctgaggag atgttctctc agttccgcat gaagatcatt aacctgaagc 400  
 tggagcggtt tcaagaccgc gtggagttct cagggaaccc cagcaagtac 450  
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 caactgctac atcatgaacc cccc 524

<210> 152

<211> 368  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 56, 123  
<223> unknown base

<400> 152  
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cctgccctgc accttcaact ccngctacac agtgaaccac aaacagttct 150  
ccctgaactg gatttaccag gagtgaaca actggctctg aggagatgtt 200  
cctccagttc ccgcatggaa gatcatttaa cctgaaagct ggaagcggtt 250  
ttcaagaacc gcgtggaagt ttctcaggga accccagcaa gtacgatgtg 300  
tcggtgatgc tgagaaacgt gcagccggag gatgagggga tttacaactg 350  
ctacatcatg aaccccc 368

<210> 153  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 153  
acggagcatg gaggtccaca gtac 24

<210> 154  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 154  
gcacgtttct cagcatcacc gac 23

<210> 155  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 155

cgctgcct gcaccttcaa ctctgctac acagtgaacc acaaacagtt 50

<210> 156

<211> 2680

<212> DNA

<213> Homo sapiens

<400> 156

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cgccgaccca gcgctcccgg ccggacgtca cccccagtg gtgctgggtcc 150  
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atgctgtaaa aaaaaaaaaa aaaaaaaaaa 2680

<210> 157

<211> 412

<212> PRT

<213> Homo Sapien

<400> 157

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Gly	Leu	Leu	Phe	Leu	Leu	Leu	Leu	Leu	Met	Leu	Leu	Ala	Asp	Pro
				20					25					30

Ala	Leu	Pro	Ala	Gly	Arg	His	Pro	Pro	Val	Val	Leu	Val	Pro	Gly
				35					40					45

Asp	Leu	Gly	Asn	Gln	Leu	Glu	Ala	Lys	Leu	Asp	Lys	Pro	Thr	Val
				50					55					60

Val	His	Tyr	Leu	Cys	Ser	Lys	Lys	Thr	Glu	Ser	Tyr	Phe	Thr	Ile
				65					70					75

Trp	Leu	Asn	Leu	Glu	Leu	Leu	Leu	Pro	Val	Ile	Ile	Asp	Cys	Trp
				80					85					90

Ile	Asp	Asn	Ile	Arg	Leu	Val	Tyr	Asn	Lys	Thr	Ser	Arg	Ala	Thr
				95					100					105

Gln	Phe	Pro	Asp	Gly	Val	Asp	Val	Arg	Val	Pro	Gly	Phe	Gly	Lys
				110					115					120

Thr	Phe	Ser	Leu	Glu	Phe	Leu	Asp	Pro	Ser	Lys	Ser	Ser	Val	Gly
				125					130					135

Ser	Tyr	Phe	His	Thr	Met	Val	Glu	Ser	Leu	Val	Gly	Trp	Gly	Tyr
				140					145					150

Thr	Arg	Gly	Glu	Asp	Val	Arg	Gly	Ala	Pro	Tyr	Asp	Trp	Arg	Arg
				155					160					165

Ala	Pro	Asn	Glu	Asn	Gly	Pro	Tyr	Phe	Leu	Ala	Leu	Arg	Glu	Met
				170					175					180

Ile	Glu	Glu	Met	Tyr	Gln	Leu	Tyr	Gly	Gly	Pro	Val	Val	Leu	Val
				185					190					195

Ala	His	Ser	Met	Gly	Asn	Met	Tyr	Thr	Leu	Tyr	Phe	Leu	Gln	Arg
				200					205					210

Gln	Pro	Gln	Ala	Trp	Lys	Asp	Lys	Tyr	Ile	Arg	Ala	Phe	Val	Ser
				215					220					225

Leu	Gly	Ala	Pro	Trp	Gly	Gly	Val	Ala	Lys	Thr	Leu	Arg	Val	Leu
				230					235					240

Ala Ser Gly Asp Asn Asn Arg Ile Pro Val Ile Gly Pro Leu Lys

245	250	255
Ile Arg Glu Gln Gln Arg Ser Ala Val	Ser Thr Ser Trp Leu	Leu
260	265	270
Pro Tyr Asn Tyr Thr Trp Ser Pro Glu	Lys Val Phe Val Gln	Thr
275	280	285
Pro Thr Ile Asn Tyr Thr Leu Arg Asp	Tyr Arg Lys Phe Phe	Gln
290	295	300
Asp Ile Gly Phe Glu Asp Gly Trp Leu	Met Arg Gln Asp Thr	Glu
305	310	315
Gly Leu Val Glu Ala Thr Met Pro Pro	Gly Val Gln Leu His	Cys
320	325	330
Leu Tyr Gly Thr Gly Val Pro Thr Pro	Asp Ser Phe Tyr Tyr	Glu
335	340	345
Ser Phe Pro Asp Arg Asp Pro Lys Ile	Cys Phe Gly Asp Gly	Asp
350	355	360
Gly Thr Val Asn Leu Lys Ser Ala Leu	Gln Cys Gln Ala Trp	Gln
365	370	375
Ser Arg Gln Glu His Gln Val Leu Leu	Gln Glu Leu Pro Gly	Ser
380	385	390
Glu His Ile Glu Met Leu Ala Asn Ala	Thr Thr Leu Ala Tyr	Leu
395	400	405
Lys Arg Val Leu Leu Gly Pro		
410		

<210> 158

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 158

ctggggctac acacggggtg agg 23

<210> 159

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 159

ggtgccgctg cagaaagtag agcg 24

<210> 160  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 160  
gccccaaatg aaaacgggcc ctacttcttg gccctccgag agatg 45

<210> 161  
<211> 1512  
<212> DNA  
<213> Homo sapiens

<400> 161  
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gcggcgcttc ctgacgcagc cgcaggtggt ggcgcgcgcc gtgtgcttgg 150  
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 tctcattcaa ag 1512

<210> 162

<211> 224

<212> PRT

<213> Homo sapiens

<400> 162

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Val	Cys	Leu	Val	Phe	Ala	Leu	Ile	Val	Phe	Ser	Cys	Ile	Tyr	Gly	35	40	45	
Glu	Gly	Tyr	Ser	Asn	Ala	His	Glu	Ser	Lys	Gln	Met	Tyr	Cys	Val	50	55	60	
Phe	Asn	Arg	Asn	Glu	Asp	Ala	Cys	Arg	Tyr	Gly	Ser	Ala	Ile	Gly	65	70	75	
Val	Leu	Ala	Phe	Leu	Ala	Ser	Ala	Phe	Phe	Leu	Val	Val	Asp	Ala	80	85	90	
Tyr	Phe	Pro	Gln	Ile	Ser	Asn	Ala	Thr	Asp	Arg	Lys	Tyr	Leu	Val	95	100	105	
Ile	Gly	Asp	Leu	Leu	Phe	Ser	Ala	Leu	Trp	Thr	Phe	Leu	Trp	Phe	110	115	120	
Val	Gly	Phe	Cys	Phe	Leu	Thr	Asn	Gln	Trp	Ala	Val	Thr	Asn	Pro	125	130	135	
Lys	Asp	Val	Leu	Val	Gly	Ala	Asp	Ser	Val	Arg	Ala	Ala	Ile	Thr	140	145	150	



Phe	Ser	Phe	Phe	Ser	Ile	Phe	Ser	Trp	Gly	Val	Leu	Ala	Ser	Leu
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Ala	Tyr	Gln	Arg	Tyr	Lys	Ala	Gly	Val	Asp	Asp	Phe	Ile	Gln	Asn
				170					175					180
Tyr	Val	Asp	Pro	Thr	Pro	Asp	Pro	Asn	Thr	Ala	Tyr	Ala	Ser	Tyr
				185					190					195
Pro	Gly	Ala	Ser	Val	Asp	Asn	Tyr	Gln	Gln	Pro	Pro	Phe	Thr	Gln
				200					205					210
Asn	Ala	Glu	Thr	Thr	Glu	Gly	Tyr	Gln	Pro	Pro	Pro	Val	Tyr	
				215					220					

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<210> 163
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 163
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<210> 164
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 164
    gtgtactgag cggcgggtag 20

<210> 165
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 165
    ctgaaggtga tggctgccct cac 23

<210> 166
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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<400> 166  
ccaggaggct catgggaaag tcc 23

<210> 167  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 167  
ccacgagtct aagcagatgt actgcgtggt caaccgcaac gaggatgcct 50

<210> 168  
<211> 3143  
<212> DNA  
<213> Homo sapiens

<400> 168  
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<210> 169

<211> 802

<212> PRT

<213> Homo sapiens

<400> 169

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			20						25					30
Cys	Glu	Asp	Ser	Lys	Arg	Lys	Ala	Arg	Gly	Tyr	Leu	Arg	Leu	Val
			35						40					45
Pro	Leu	Phe	Val	Leu	Leu	Ala	Leu	Leu	Val	Leu	Ala	Ser	Ala	Gly
			50						55					60
Val	Leu	Leu	Trp	Tyr	Phe	Leu	Gly	Tyr	Lys	Ala	Glu	Val	Met	Val
			65						70					75
Ser	Gln	Val	Tyr	Ser	Gly	Ser	Leu	Arg	Val	Leu	Asn	Arg	His	Phe
			80						85					90
Ser	Gln	Asp	Leu	Thr	Arg	Arg	Glu	Ser	Ser	Ala	Phe	Arg	Ser	Glu

95					100					105				
Thr	Ala	Lys	Ala	Gln	Lys	Met	Leu	Lys	Glu	Leu	Ile	Thr	Ser	Thr
				110					115					120
Arg	Leu	Gly	Thr	Tyr	Tyr	Asn	Ser	Ser	Ser	Val	Tyr	Ser	Phe	Gly
				125					130					135
Glu	Gly	Pro	Leu	Thr	Cys	Phe	Phe	Trp	Phe	Ile	Leu	Gln	Ile	Pro
				140					145					150
Glu	His	Arg	Arg	Leu	Met	Leu	Ser	Pro	Glu	Val	Val	Gln	Ala	Leu
				155					160					165
Leu	Val	Glu	Glu	Leu	Leu	Ser	Thr	Val	Asn	Ser	Ser	Ala	Ala	Val
				170					175					180
Pro	Tyr	Arg	Ala	Glu	Tyr	Glu	Val	Asp	Pro	Glu	Gly	Leu	Val	Ile
				185					190					195
Leu	Glu	Ala	Ser	Val	Lys	Asp	Ile	Ala	Ala	Leu	Asn	Ser	Thr	Leu
				200					205					210
Gly	Cys	Tyr	Arg	Tyr	Ser	Tyr	Val	Gly	Gln	Gly	Gln	Val	Leu	Arg
				215					220					225
Leu	Lys	Gly	Pro	Asp	His	Leu	Ala	Ser	Ser	Cys	Leu	Trp	His	Leu
				230					235					240
Gln	Gly	Pro	Lys	Asp	Leu	Met	Leu	Lys	Leu	Arg	Leu	Glu	Trp	Thr
				245					250					255
Leu	Ala	Glu	Cys	Arg	Asp	Arg	Leu	Ala	Met	Tyr	Asp	Val	Ala	Gly
				260					265					270
Pro	Leu	Glu	Lys	Arg	Leu	Ile	Thr	Ser	Val	Tyr	Gly	Cys	Ser	Arg
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Gln	Glu	Pro	Val	Val	Glu	Val	Leu	Ala	Ser	Gly	Ala	Ile	Met	Ala
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Val	Val	Trp	Lys	Lys	Gly	Leu	His	Ser	Tyr	Tyr	Asp	Pro	Phe	Val
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Leu	Ser	Val	Gln	Pro	Val	Val	Phe	Gln	Ala	Cys	Glu	Val	Asn	Leu
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Thr	Leu	Asp	Asn	Arg	Leu	Asp	Ser	Gln	Gly	Val	Leu	Ser	Thr	Pro
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Tyr	Phe	Pro	Ser	Tyr	Tyr	Ser	Pro	Gln	Thr	His	Cys	Ser	Trp	His
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Leu	Thr	Val	Pro	Ser	Leu	Asp	Tyr	Gly	Leu	Ala	Leu	Trp	Phe	Asp
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Ile	Thr	Ile	Asn	Phe	Thr	Ser	Gln	Ile	Ser	Leu	Thr	Gly	Pro	Gly
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Ser	Asp	Glu	Glu	Gln	Cys	Gln	Glu	Gly	Val	Pro	Cys	Gly	Thr	Phe
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Gln	Val	Arg	Gly	Arg	His	Ile	Cys	Gly	Gly	Ala	Leu	Ile	Ala	Asp
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Arg	Trp	Val	Ile	Thr	Ala	Ala	His	Cys	Phe	Gln	Glu	Asp	Ser	Met
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Ala	Ser	Thr	Val	Leu	Trp	Thr	Val	Phe	Leu	Gly	Lys	Val	Trp	Gln
				620					625					630
Asn	Ser	Arg	Trp	Pro	Gly	Glu	Val	Ser	Phe	Lys	Val	Ser	Arg	Leu
				635					640					645
Leu	Leu	His	Pro	Tyr	His	Glu	Glu	Asp	Ser	His	Asp	Tyr	Asp	Val
				650					655					660
Ala	Leu	Leu	Gln	Leu	Asp	His	Pro	Val	Val	Arg	Ser	Ala	Ala	Val

665	670	675
Arg Pro Val Cys Leu Pro Ala Arg Ser	His Phe Phe Glu Pro Gly	
680	685	690
Leu His Cys Trp Ile Thr Gly Trp Gly	Ala Leu Arg Glu Gly Gly	
695	700	705
Pro Ile Ser Asn Ala Leu Gln Lys Val	Asp Val Gln Leu Ile Pro	
710	715	720
Gln Asp Leu Cys Ser Glu Ala Tyr Arg	Tyr Gln Val Thr Pro Arg	
725	730	735
Met Leu Cys Ala Gly Tyr Arg Lys Gly	Lys Lys Asp Ala Cys Gln	
740	745	750
Gly Asp Ser Gly Gly Pro Leu Val Cys	Lys Ala Leu Ser Gly Arg	
755	760	765
Trp Phe Leu Ala Gly Leu Val Ser Trp	Gly Leu Gly Cys Gly Arg	
770	775	780
Pro Asn Tyr Phe Gly Val Tyr Thr Arg	Ile Thr Gly Val Ile Ser	
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Trp Ile Gln Gln Val Val Thr		
800		

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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 171

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<210> 172

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 172

taatccagca gtgcaggccg gg 22

<210> 173

<211> 50

<212> DNA



<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<210> 174

<211> 25

<212> DNA

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<223> Synthetic oligonucleotide probe

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<210> 176

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<213> Artificial Sequence

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<400> 176

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<210> 177

<211> 1510

<212> DNA

<213> Homo sapiens

<400> 177

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gctggaaaca ccaagaggtg gtttttgttt tttaaaactt ctgtttcttg 200

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<210> 178  
<211> 354  
<212> PRT  
<213> Homo sapiens

<400> 178

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Cys	Phe	Ala	Ala	Gly	Ser	Pro	Val	Pro	Phe	Gly	Pro	Glu	Gly	Arg
				20					25					30
Leu	Glu	Asp	Lys	Leu	His	Lys	Pro	Lys	Ala	Thr	Gln	Thr	Glu	Val
				35					40					45
Lys	Pro	Ser	Val	Arg	Phe	Asn	Leu	Arg	Thr	Ser	Lys	Asp	Pro	Glu
				50					55					60
His	Glu	Gly	Cys	Tyr	Leu	Ser	Val	Gly	His	Ser	Gln	Pro	Leu	Glu
				65					70					75
Asp	Cys	Ser	Phe	Asn	Met	Thr	Ala	Lys	Thr	Phe	Phe	Ile	Ile	His
				80					85					90
Gly	Trp	Thr	Met	Ser	Gly	Ile	Phe	Glu	Asn	Trp	Leu	His	Lys	Leu
				95					100					105
Val	Ser	Ala	Leu	His	Thr	Arg	Glu	Lys	Asp	Ala	Asn	Val	Val	Val
				110					115					120
Val	Asp	Trp	Leu	Pro	Leu	Ala	His	Gln	Leu	Tyr	Thr	Asp	Ala	Val
				125					130					135
Asn	Asn	Thr	Arg	Val	Val	Gly	His	Ser	Ile	Ala	Arg	Met	Leu	Asp
				140					145					150
Trp	Leu	Gln	Glu	Lys	Asp	Asp	Phe	Ser	Leu	Gly	Asn	Val	His	Leu
				155					160					165
Ile	Gly	Tyr	Ser	Leu	Gly	Ala	His	Val	Ala	Gly	Tyr	Ala	Gly	Asn
				170					175					180
Phe	Val	Lys	Gly	Thr	Val	Gly	Arg	Ile	Thr	Gly	Leu	Asp	Pro	Ala
				185					190					195
Gly	Pro	Met	Phe	Glu	Gly	Ala	Asp	Ile	His	Lys	Arg	Leu	Ser	Pro
				200					205					210
Asp	Asp	Ala	Asp	Phe	Val	Asp	Val	Leu	His	Thr	Tyr	Thr	Arg	Ser
				215					220					225
Phe	Gly	Leu	Ser	Ile	Gly	Ile	Gln	Met	Pro	Val	Gly	His	Ile	Asp
				230					235					240
Ile	Tyr	Pro	Asn	Gly	Gly	Asp	Phe	Gln	Pro	Gly	Cys	Gly	Leu	Asn
				245					250					255
Asp	Val	Leu	Gly	Ser	Ile	Ala	Tyr	Gly	Thr	Ile	Thr	Glu	Val	Val
				260					265					270
Lys	Cys	Glu	His	Glu	Arg	Ala	Val	His	Leu	Phe	Val	Asp	Ser	Leu
				275					280					285

Val Asn Gln Asp Lys Pro Ser Phe Ala Phe Gln Cys Thr Asp Ser  
290 295 300

Asn Arg Phe Lys Lys Gly Ile Cys Leu Ser Cys Arg Lys Asn Arg  
305 310 315

Cys Asn Ser Ile Gly Tyr Asn Ala Lys Lys Met Arg Asn Lys Arg  
320 325 330

Asn Ser Lys Met Tyr Leu Lys Thr Arg Ala Gly Met Pro Phe Arg  
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Gly Asn Leu Gln Ser Leu Glu Cys Pro  
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<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 179

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<212> DNA

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<223> Synthetic oligonucleotide probe

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<210> 181

<211> 44

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 181

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<210> 182

<211> 3240

<212> DNA

<213> Homo sapiens

<400> 182

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<210> 183
<211> 713
<212> PRT
<213> Homo sapiens

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 1                5                10                15

Ala His Pro Asp Arg Ile Ile Phe Pro Asn His Ala Cys Glu Asp
      20                25                .                30

Pro Pro Ala Val Leu Leu Glu Val Gln Gly Thr Leu Gln Arg Pro
      35                40                45

Leu Val Arg Asp Ser Arg Thr Ser Pro Ala Asn Cys Thr Trp Leu
      50                55                60

Ile Leu Gly Ser Lys Glu Gln Thr Val Thr Ile Arg Phe Gln Lys
      65                70                75

Leu His Leu Ala Cys Gly Ser Glu Arg Leu Thr Leu Arg Ser Pro
      80                85                90

Leu Gln Pro Leu Ile Ser Leu Cys Glu Ala Pro Pro Ser Pro Leu
      95                100               105

Gln Leu Pro Gly Gly Asn Val Thr Ile Thr Tyr Ser Tyr Ala Gly
     110               115               120

Ala Arg Ala Pro Met Gly Gln Gly Phe Leu Leu Ser Tyr Ser Gln
     125               130               135

Asp Trp Leu Met Cys Leu Gln Glu Glu Phe Gln Cys Leu Asn His
     140               145               150

Arg Cys Val Ser Ala Val Gln Arg Cys Asp Gly Val Asp Ala Cys
     155               160               165

Gly Asp Gly Ser Asp Glu Ala Gly Cys Ser Ser Asp Pro Phe Pro
     170               175               180

Gly Leu Thr Pro Arg Pro Val Pro Ser Leu Pro Cys Asn Val Thr

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185										190					195				
Leu	Glu	Asp	Phe	Tyr	Gly	Val	Phe	Ser	Ser	Pro	Gly	Tyr	Thr	His					
				200					205					210					
Leu	Ala	Ser	Val	Ser	His	Pro	Gln	Ser	Cys	His	Trp	Leu	Leu	Asp					
				215					220					225					
Pro	His	Asp	Gly	Arg	Arg	Leu	Ala	Val	Arg	Phe	Thr	Ala	Leu	Asp					
				230					235					240					
Leu	Gly	Phe	Gly	Asp	Ala	Val	His	Val	Tyr	Asp	Gly	Pro	Gly	Pro					
				245					250					255					
Pro	Glu	Ser	Ser	Arg	Leu	Leu	Arg	Ser	Leu	Thr	His	Phe	Ser	Asn					
				260					265					270					
Gly	Lys	Ala	Val	Thr	Val	Glu	Thr	Leu	Ser	Gly	Gln	Ala	Val	Val					
				275					280					285					
Ser	Tyr	His	Thr	Val	Ala	Trp	Ser	Asn	Gly	Arg	Gly	Phe	Asn	Ala					
				290					295					300					
Thr	Tyr	His	Val	Arg	Gly	Tyr	Cys	Leu	Pro	Trp	Asp	Arg	Pro	Cys					
				305					310					315					
Gly	Leu	Gly	Ser	Gly	Leu	Gly	Ala	Gly	Glu	Gly	Leu	Gly	Glu	Arg					
				320					325					330					
Cys	Tyr	Ser	Glu	Ala	Gln	Arg	Cys	Asp	Gly	Ser	Trp	Asp	Cys	Ala					
				335					340					345					
Asp	Gly	Thr	Asp	Glu	Glu	Asp	Cys	Pro	Gly	Cys	Pro	Pro	Gly	His					
				350					355					360					
Phe	Pro	Cys	Gly	Ala	Ala	Gly	Thr	Ser	Gly	Ala	Thr	Ala	Cys	Tyr					
				365					370					375					
Leu	Pro	Ala	Asp	Arg	Cys	Asn	Tyr	Gln	Thr	Phe	Cys	Ala	Asp	Gly					
				380					385					390					
Ala	Asp	Glu	Arg	Arg	Cys	Arg	His	Cys	Gln	Pro	Gly	Asn	Phe	Arg					
				395					400					405					
Cys	Arg	Asp	Glu	Lys	Cys	Val	Tyr	Glu	Thr	Trp	Val	Cys	Asp	Gly					
				410					415					420					
Gln	Pro	Asp	Cys	Ala	Asp	Gly	Ser	Asp	Glu	Trp	Asp	Cys	Ser	Tyr					
				425					430					435					
Val	Leu	Pro	Arg	Lys	Val	Ile	Thr	Ala	Ala	Val	Ile	Gly	Ser	Leu					
				440					445					450					
Val	Cys	Gly	Leu	Leu	Leu	Val	Ile	Ala	Leu	Gly	Cys	Thr	Cys	Lys					
				455					460					465					
Leu	Tyr	Ala	Ile	Arg	Thr	Gln	Glu	Tyr	Ser	Ile	Phe	Ala	Pro	Leu					



470	475	480
Ser Arg Met Glu Ala Glu Ile Val Gln	Gln Gln Ala Pro Pro	Ser
485	490	495
Tyr Gly Gln Leu Ile Ala Gln Gly Ala	Ile Pro Pro Val Glu	Asp
500	505	510
Phe Pro Thr Glu Asn Pro Asn Asp Asn	Ser Val Leu Gly Asn	Leu
515	520	525
Arg Ser Leu Leu Gln Ile Leu Arg Gln	Asp Met Thr Pro Gly	Gly
530	535	540
Gly Pro Gly Ala Arg Arg Arg Gln Arg	Gly Arg Leu Met Arg	Arg
545	550	555
Leu Val Arg Arg Leu Arg Arg Trp Gly	Leu Leu Pro Arg Thr	Asn
560	565	570
Thr Pro Ala Arg Ala Ser Glu Ala Arg	Ser Gln Val Thr Pro	Ser
575	580	585
Ala Ala Pro Leu Glu Ala Leu Asp Gly	Gly Thr Gly Pro Ala	Arg
590	595	600
Glu Gly Gly Ala Val Gly Gly Gln Asp	Gly Glu Gln Ala Pro	Pro
605	610	615
Leu Pro Ile Lys Ala Pro Leu Pro Ser	Ala Ser Thr Ser Pro	Ala
620	625	630
Pro Thr Thr Val Pro Glu Ala Pro Gly	Pro Leu Pro Ser Leu	Pro
635	640	645
Leu Glu Pro Ser Leu Leu Ser Gly Val	Val Gln Ala Leu Arg	Gly
650	655	660
Arg Leu Leu Pro Ser Leu Gly Pro Pro	Gly Pro Thr Arg Ser	Pro
665	670	675
Pro Gly Pro His Thr Ala Val Leu Ala	Leu Glu Asp Glu Asp	Asp
680	685	690
Val Leu Leu Val Pro Leu Ala Glu Pro	Gly Val Trp Val Ala	Glu
695	700	705
Ala Glu Asp Glu Pro Leu Leu Thr		
710		

<210> 184

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 184  
ggctgtcact gtggagacac 20

<210> 185  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 185  
gcaaggtcat tacagctg 18

<210> 186  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 186  
agaacatagg agcagtccca ctc 23

<210> 187  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 187  
tgctgtctgc tgcacaatct cag 23

<210> 188  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 188  
ggctattgct tgccttggga cagaccctgt ggcttaggct ctggc 45

<210> 189  
<211> 663  
<212> DNA  
<213> Homo sapiens

<400> 189  
cgagctgggc gagaagtagg ggagggcggt gctccgccgc ggtggcggtt 50  
  
gctatcgctt cgcagaacct actcaggcag ccagctgaga agagttgagg 100

gaaagtgctg ctgctgggtc tgcagacgcg atggataacg tgcagccgaa 150  
 aataaaacat cgccccttct gcttcagtgt gaaaggccac gtgaagatgc 200  
 tgcggctggc actaactgtg acatctatga ccttttttat catcgcacaa 250  
 gcccctgaac catatattgt tatcactgga tttgaagtca ccgttatctt 300  
 atttttcata cttttatatg tactcagact tgatcgatta atgaagtggg 350  
 tattttggcc tttgcttgat attatcaact cactggtaac aacagtattc 400  
 atgctcatcg tatctgtgtt ggcaactgata ccagaaacca caacattgac 450  
 agttgggtgga ggggtgtttg cacttgtgac agcagtatgc tgtcttgccg 500  
 acggggccct tatttaccgg aagcttctgt tcaatcccag cggtccttac 550  
 cagaaaaagc ctgtgcatga aaaaaaagaa gttttgtaat tttatattac 600  
 tttttagttt gatactaagt attaaacata tttctgtatt cttccaaaaa 650  
 aaaaaaaaaa aaa 663

<210> 190  
 <211> 152  
 <212> PRT  
 <213> Homo sapiens

<400> 190  
 Met Asp Asn Val Gln Pro Lys Ile Lys His Arg Pro Phe Cys Phe  
 1 5 10 15  
 Ser Val Lys Gly His Val Lys Met Leu Arg Leu Ala Leu Thr Val  
 20 25 30  
 Thr Ser Met Thr Phe Phe Ile Ile Ala Gln Ala Pro Glu Pro Tyr  
 35 40 45  
 Ile Val Ile Thr Gly Phe Glu Val Thr Val Ile Leu Phe Phe Ile  
 50 55 60  
 Leu Leu Tyr Val Leu Arg Leu Asp Arg Leu Met Lys Trp Leu Phe  
 65 70 75  
 Trp Pro Leu Leu Asp Ile Ile Asn Ser Leu Val Thr Thr Val Phe  
 80 85 90  
 Met Leu Ile Val Ser Val Leu Ala Leu Ile Pro Glu Thr Thr Thr  
 95 100 105  
 Leu Thr Val Gly Gly Gly Val Phe Ala Leu Val Thr Ala Val Cys  
 110 115 120  
 Cys Leu Ala Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu Phe Asn  
 125 130 135

Pro Ser Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys Glu  
140 145 150

Val Leu

<210> 191  
<211> 495  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 78, 212, 234, 487  
<223> unknown base

<400> 191  
gggcgagaag taggggaggg cgtgttccgc cgcggtggcg gttgctatcg 50  
ttttgcagaa cctactcagg cagccagntg agaagagttg agggaaagtg 100  
ctgctgctgg gtctgcagac gcgatggata acgtgcagcc gaaaataaaa 150  
catcgcccct tctgcttcag tgtgaaaggc cacgtgaaga tgctgcggct 200  
ggcactaact gngacatcta tgaccttttt tatnatcgca caagcccctg 250  
aaccatatat tgttatcact ggatttgaag tcaccgttat cttatttttc 300  
atacttttat atgtactcag acttgatcga ttaatgaagt ggttattttg 350  
gcctttgctt gatattatca actcactggg aacaacagta ttcatgctca 400  
tsgtatctgt gttggcactg ataccagaaa ccacaacatt gacagttggt 450  
ggaggggtgt ttgcacttgt gacagcagta tgctgtnttg ccgac 495

<210> 192  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 192  
cgttttgcag aacctactca ggcag 25

<210> 193  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 193  
cctccaccaa ctgtcaatgt tgtgg 25

<210> 194  
<211> 40  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 194  
aaagtgtctg tgctgggtct gcagacgcga tggataacgt 40

<210> 195  
<211> 1879  
<212> DNA  
<213> Homo sapien

<400> 195  
cagccccgcg cgccggccga gtcgtgagc cgcggtgcc ggacgggacg 50  
ggaccggcta ggctgggcgc gcccccgagg ccccgccgtg ggcatgggcg 100  
cactggcccc ggcgctgctg ctgcctctgc tggcccagtg gtcctgcgc 150  
gccgccccgg agctggcccc cgcgcccttc acgtgcccc tccgggtggc 200  
cgcgggccacg aaccgcgtag ttgcgcccac cccgggaccc gggacccctg 250  
ccgagcgcca cgccgacggc ttggcgctcg ccctggagcc tgcctggcg 300  
tccccgcggg gcgccgccaa cttcttgccc atggtagaca acctgcaggg 350  
ggactctggc cgcggtact acctggagat gctgatcggg accccccgc 400  
agaagctaca gattctcgtt gacactggaa gcagtaactt tgccgtggca 450  
ggaacccgc actcctacat agacacgtac tttgacacag agaggtctag 500  
cacataccgc tccaagggct ttgacgtcac agtgaagtac acacaaggaa 550  
gctggacggg cttcggtggg gaagacctcg tcaccatccc caaaggcttc 600  
aatacttctt ttcttgtcaa cattgccact atttttgaat cagagaattt 650  
ctttttgcct gggattaaat ggaatggaat acttggccta gcttatgcca 700  
cacttgccaa gccatcaagt tctctggaga ccttcttcga ctccctggtg 750  
acacaagcaa acatcccaa cgttttctcc atgcagatgt gtggagccgg 800  
cttgcccggt gctggatctg ggaccaacgg aggtagtctt gtcttggtg 850  
gaattgaacc aagtttgtat aaaggagaca tctggtatac ccctattaag 900  
gaagagtggg actaccagat agaaattctg aaattggaaa ttggaggcca 950

aagccttaat ctggactgca gagagtataa cgcagacaag gccatcgtgg 1000  
acagtggcac cacgctgctg cgcctgcccc agaaggtggt tgatgcggtg 1050  
gtggaagctg tggcccgcgc atctctgatt ccagaattct ctgatgggtt 1100  
ctggactggg tcccagctgg cgtgctggac gaattcggaa acaccttgg 1150  
cttacttccc taaaatctcc atctacctga gagacgagaa ctccagcagg 1200  
tcattccgta tcacaatcct gcctcagctt tacattcagc ccatgatggg 1250  
ggccggcctg aattatgaat gttaccgatt cggcatttcc ccatccacaa 1300  
atgcgctggt gatcggtgcc acggtgatgg agggcttcta cgtcatcttc 1350  
gacagagccc agaagagggg gggcttcgca gcgagcccct gtgcagaaat 1400  
tgcagggtgct gcagtgtctg aaatttccgg gcctttctca acagaggatg 1450  
tagccagcaa ctgtgtcccc gtcagttctt tgagcgagcc cattttgtgg 1500  
attgtgtcct atgcgctcat gagcgtctgt ggagccatcc tccttgtctt 1550  
aatcgtcctg ctgctgctgc cgttccggtg tcagcgtcgc ccccgtagcc 1600  
ctgagggtcgt caatgatgag tcctctctgg tcagacatcg ctggaaatga 1650  
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acatttccag ggcagcagcc gggatcgatg gtggcgcttt ctctgtgcc 1750  
caccgctctt caatctctgt tctgctccca gatgccttct agattcactg 1800  
tcttttgatt cttgattttc aagctttcaa atcctcccta cttccaagaa 1850  
aaataattaa aaaaaaaact tcattctaa 1879

<210> 196  
<211> 518  
<212> PRT  
<213> Homo sapien

<400> 196  
Met Gly Ala Leu Ala Arg Ala Leu Leu Leu Pro Leu Leu Ala Gln  
1 5 10 15  
Trp Leu Leu Arg Ala Ala Pro Glu Leu Ala Pro Ala Pro Phe Thr  
20 25 30  
Leu Pro Leu Arg Val Ala Ala Ala Thr Asn Arg Val Val Ala Pro  
35 40 45  
Thr Pro Gly Pro Gly Thr Pro Ala Glu Arg His Ala Asp Gly Leu  
50 55 60

Ala	Leu	Ala	Leu	Glu	Pro	Ala	Leu	Ala	Ser	Pro	Ala	Gly	Ala	Ala		65	70	75
Asn	Phe	Leu	Ala	Met	Val	Asp	Asn	Leu	Gln	Gly	Asp	Ser	Gly	Arg		80	85	90
Gly	Tyr	Tyr	Leu	Glu	Met	Leu	Ile	Gly	Thr	Pro	Pro	Gln	Lys	Leu		95	100	105
Gln	Ile	Leu	Val	Asp	Thr	Gly	Ser	Ser	Asn	Phe	Ala	Val	Ala	Gly		110	115	120
Thr	Pro	His	Ser	Tyr	Ile	Asp	Thr	Tyr	Phe	Asp	Thr	Glu	Arg	Ser		125	130	135
Ser	Thr	Tyr	Arg	Ser	Lys	Gly	Phe	Asp	Val	Thr	Val	Lys	Tyr	Thr		140	145	150
Gln	Gly	Ser	Trp	Thr	Gly	Phe	Val	Gly	Glu	Asp	Leu	Val	Thr	Ile		155	160	165
Pro	Lys	Gly	Phe	Asn	Thr	Ser	Phe	Leu	Val	Asn	Ile	Ala	Thr	Ile		170	175	180
Phe	Glu	Ser	Glu	Asn	Phe	Phe	Leu	Pro	Gly	Ile	Lys	Trp	Asn	Gly		185	190	195
Ile	Leu	Gly	Leu	Ala	Tyr	Ala	Thr	Leu	Ala	Lys	Pro	Ser	Ser	Ser		200	205	210
Leu	Glu	Thr	Phe	Phe	Asp	Ser	Leu	Val	Thr	Gln	Ala	Asn	Ile	Pro		215	220	225
Asn	Val	Phe	Ser	Met	Gln	Met	Cys	Gly	Ala	Gly	Leu	Pro	Val	Ala		230	235	240
Gly	Ser	Gly	Thr	Asn	Gly	Gly	Ser	Leu	Val	Leu	Gly	Gly	Ile	Glu		245	250	255
Pro	Ser	Leu	Tyr	Lys	Gly	Asp	Ile	Trp	Tyr	Thr	Pro	Ile	Lys	Glu		260	265	270
Glu	Trp	Tyr	Tyr	Gln	Ile	Glu	Ile	Leu	Lys	Leu	Glu	Ile	Gly	Gly		275	280	285
Gln	Ser	Leu	Asn	Leu	Asp	Cys	Arg	Glu	Tyr	Asn	Ala	Asp	Lys	Ala		290	295	300
Ile	Val	Asp	Ser	Gly	Thr	Thr	Leu	Leu	Arg	Leu	Pro	Gln	Lys	Val		305	310	315
Phe	Asp	Ala	Val	Val	Glu	Ala	Val	Ala	Arg	Ala	Ser	Leu	Ile	Pro		320	325	330
Glu	Phe	Ser	Asp	Gly	Phe	Trp	Thr	Gly	Ser	Gln	Leu	Ala	Cys	Trp		335	340	345

Thr Asn Ser Glu Thr Pro Trp Ser Tyr Phe Pro Lys Ile Ser Ile	350	355	360
Tyr Leu Arg Asp Glu Asn Ser Ser Arg Ser Phe Arg Ile Thr Ile	365	370	375
Leu Pro Gln Leu Tyr Ile Gln Pro Met Met Gly Ala Gly Leu Asn	380	385	390
Tyr Glu Cys Tyr Arg Phe Gly Ile Ser Pro Ser Thr Asn Ala Leu	395	400	405
Val Ile Gly Ala Thr Val Met Glu Gly Phe Tyr Val Ile Phe Asp	410	415	420
Arg Ala Gln Lys Arg Val Gly Phe Ala Ala Ser Pro Cys Ala Glu	425	430	435
Ile Ala Gly Ala Ala Val Ser Glu Ile Ser Gly Pro Phe Ser Thr	440	445	450
Glu Asp Val Ala Ser Asn Cys Val Pro Ala Gln Ser Leu Ser Glu	455	460	465
Pro Ile Leu Trp Ile Val Ser Tyr Ala Leu Met Ser Val Cys Gly	470	475	480
Ala Ile Leu Leu Val Leu Ile Val Leu Leu Leu Pro Phe Arg	485	490	495
Cys Gln Arg Arg Pro Arg Asp Pro Glu Val Val Asn Asp Glu Ser	500	505	510
Ser Leu Val Arg His Arg Trp Lys	515		

<210> 197

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 197

cgcagaagct acagattctc g 21

<210> 198

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 198

ggaaattgga ggccaaagc 19



<210> 199  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 199  
ggatgtagcc agcaactgtg 20

<210> 200  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 200  
gccttggtc gttctcttc 19

<210> 201  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 201  
gtcctgtgc ctggatgg 18

<210> 202  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 202  
gacaagacta cctccgttgg tc 22

<210> 203  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 203  
tgatgcacag ttcagcacct gttg 24

<210> 204

<211> 47  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 204  
cgctccaagg gctttgacgt cacagtgaag tacacacaag gaagctg 47

<210> 205  
<211> 1939  
<212> DNA  
<213> Homo sapiens

<400> 205  
cgctccgcc ttcggaggct gacgcgcccg ggcgcggttc caggcctgtg 50  
cagggcggat cggcagccgc ctggcggcga tccagggcgg tgcggggcct 100  
gggcgggagc cgggaggcgc ggccggcatg gaggcgctgc tgctgggcgc 150  
ggggttgctg ctgggcgctt acgtgcttgt ctactacaac ctggtgaagg 200  
ccccgcgctg cggcggcatg ggcaacctgc ggggcgcgac ggccgtggtc 250  
acgggcgcca acagcggcat cggaaagatg acggcgctgg agctggcgcg 300  
ccggggagcg cgcgtggtgc tggcctgccg cagccaggag cgcggggagg 350  
cggtgcctt cgacctccgc caggagagtg ggaacaatga ggtcatcttc 400  
atggccttgg acttggccag tctggcctcg gtgcgggcct ttgccactgc 450  
ctttctgagc tctgagccac ggttgacat cctcatccac aatgccggtg 500  
tcagttcctg tggccggacc cgtgaggcgt ttaacctgct gcttcgggtg 550  
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caggagctgc gggcatatgc tgacactaag ctggctaata tactgtttgc 750  
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 gaggagccca cagtttctca accttacccc agccctcaga gctcaccaga 1200  
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 ttgaaaacct cggatgtgtg tgaggccatg ccctggacac tgacgggttt 1350  
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 tctcggaat ttggatgtag tattttcagg cccaccctt attgattctg 1550  
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 attgagaatt agtgaactga tccctttgca accgtctagc taggtagtta 1650  
 aattaccccc atgttaatga agcgggaatta ggctcccgag ctaagggact 1700  
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 cagggcaggg cagctggtat cgaggtgcc catgggagta aggggacgcc 1850  
 ttccgggagg atgcagggt ggggtcatct gtatctgaag cccctcggaa 1900  
 taaagcgcgt tgaccgcaa aaaaaaaaaa aaaaaaaaaa 1939

<210> 206  
 <211> 377  
 <212> PRT  
 <213> Homo sapiens

<400> 206  
 Met Glu Ala Leu Leu Leu Gly Ala Gly Leu Leu Leu Gly Ala Tyr  
 1 5 10 15  
 Val Leu Val Tyr Tyr Asn Leu Val Lys Ala Pro Pro Cys Gly Gly  
 20 25 30  
 Met Gly Asn Leu Arg Gly Arg Thr Ala Val Val Thr Gly Ala Asn  
 35 40 45  
 Ser Gly Ile Gly Lys Met Thr Ala Leu Glu Leu Ala Arg Arg Gly  
 50 55 60  
 Ala Arg Val Val Leu Ala Cys Arg Ser Gln Glu Arg Gly Glu Ala  
 65 70 75

Ala	Ala	Phe	Asp	Leu	Arg	Gln	Glu	Ser	Gly	Asn	Asn	Glu	Val	Ile	80	85	90
Phe	Met	Ala	Leu	Asp	Leu	Ala	Ser	Leu	Ala	Ser	Val	Arg	Ala	Phe	95	100	105
Ala	Thr	Ala	Phe	Leu	Ser	Ser	Glu	Pro	Arg	Leu	Asp	Ile	Leu	Ile	110	115	120
His	Asn	Ala	Gly	Ile	Ser	Ser	Cys	Gly	Arg	Thr	Arg	Glu	Ala	Phe	125	130	135
Asn	Leu	Leu	Leu	Arg	Val	Asn	His	Ile	Gly	Pro	Phe	Leu	Leu	Thr	140	145	150
His	Leu	Leu	Leu	Pro	Cys	Leu	Lys	Ala	Cys	Ala	Pro	Ser	Arg	Val	155	160	165
Val	Val	Val	Ala	Ser	Ala	Ala	His	Cys	Arg	Gly	Arg	Leu	Asp	Phe	170	175	180
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Ala	Tyr	Ala	Asp	Thr	Lys	Leu	Ala	Asn	Val	Leu	Phe	Ala	Arg	Glu	200	205	210
Leu	Ala	Asn	Gln	Leu	Glu	Ala	Thr	Gly	Val	Thr	Cys	Tyr	Ala	Ala	215	220	225
His	Pro	Gly	Pro	Val	Asn	Ser	Glu	Leu	Phe	Leu	Arg	His	Val	Pro	230	235	240
Gly	Trp	Leu	Arg	Pro	Leu	Leu	Arg	Pro	Leu	Ala	Trp	Leu	Val	Leu	245	250	255
Arg	Ala	Pro	Arg	Gly	Gly	Ala	Gln	Thr	Pro	Leu	Tyr	Cys	Ala	Leu	260	265	270
Gln	Glu	Gly	Ile	Glu	Pro	Leu	Ser	Gly	Arg	Tyr	Phe	Ala	Asn	Cys	275	280	285
His	Val	Glu	Glu	Val	Pro	Pro	Ala	Ala	Arg	Asp	Asp	Arg	Ala	Ala	290	295	300
His	Arg	Leu	Trp	Glu	Ala	Ser	Lys	Arg	Leu	Ala	Gly	Leu	Gly	Pro	305	310	315
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Glu	Ala	Pro	Ser	Ser	Leu	Ser	Thr	Pro	His	Pro	Glu	Glu	Pro	Thr	335	340	345
Val	Ser	Gln	Pro	Tyr	Pro	Ser	Pro	Gln	Ser	Ser	Pro	Asp	Leu	Ser	350	355	360

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Cys Gln Ala Ser Gly Gln Pro Pro Pro Thr Ile Arg Trp Leu Leu
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Asn Gly Gln Pro Leu Ser Met Val Pro Pro Asp Pro His His Leu
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Leu Pro Asp Gly Thr Leu Leu Leu Leu Gln Pro Pro Ala Arg Gly
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His Ala His Asp Gly Gln Ala Leu Ser Thr Asp Leu Gly Val Tyr
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Thr Cys Glu Ala Ser Asn Arg Leu Gly Thr Ala Val Ser Arg Gly
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Ala Arg Leu Ser Val Ala Val Leu Arg Glu Asp Phe Gln Ile Gln
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Glu Pro Val Glu	Leu Leu Ala Val Arg	Ile Gln Leu Glu Asn	Val
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Ala Glu Leu Gly	Gly Leu His Trp Gly	Gln Asp Tyr Glu Phe	Lys
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Glu Val Thr Leu	Lys Pro Gly Asn Gly	Thr Val Phe Val Ser	Trp
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Val Pro Pro Pro	Ala Glu Asn His Asn	Gly Ile Ile Arg Gly	Tyr
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Ala Gly Glu Pro	Ser Arg Pro Val Cys	Leu Leu Leu Glu Gln	Ala
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Thr	Cys	Gly	Val	Ala	Leu	Trp	Leu	Leu	Leu	Leu	Gly	Thr	Ala	Val		455	460	465
Cys	Ile	His	Arg	Arg	Arg	Arg	Ala	Arg	Val	His	Leu	Gly	Pro	Gly		470	475	480
Leu	Tyr	Arg	Tyr	Thr	Ser	Glu	Asp	Ala	Ile	Leu	Lys	His	Arg	Met		485	490	495
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Leu	Gly	Ala	Asp	Ala	Arg	Asp	Pro	Leu	Asp	Cys	Arg	Arg	Ser	Leu		530	535	540
Leu	Ser	Trp	Asp	Ser	Arg	Ser	Pro	Gly	Val	Pro	Leu	Leu	Pro	Asp		545	550	555
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Thr	Pro	Ala	Arg	Pro	Ser	Pro	Gln	Val	Pro	Ala	Val	Arg	Arg	Leu		575	580	585
Pro	Pro	Gln	Leu	Ala	Gln	Leu	Ser	Ser	Pro	Cys	Ser	Ser	Ser	Asp		590	595	600
Ser	Leu	Cys	Ser	Arg	Arg	Gly	Leu	Ser	Ser	Pro	Arg	Leu	Ser	Leu		605	610	615
Ala	Pro	Ala	Glu	Ala	Trp	Lys	Ala	Lys	Lys	Lys	Gln	Glu	Leu	Gln		620	625	630
His	Ala	Asn	Ser	Ser	Pro	Leu	Leu	Arg	Gly	Ser	His	Ser	Leu	Glu		635	640	645
Leu	Arg	Ala	Cys	Glu	Leu	Gly	Asn	Arg	Gly	Ser	Lys	Asn	Leu	Ser		650	655	660
Gln	Ser	Pro	Gly	Ala	Val	Pro	Gln	Ala	Leu	Val	Ala	Trp	Arg	Ala		665	670	675
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His	Leu	Pro	Pro	Ala	Pro	Leu	Phe	Pro	His	Glu	Thr	Pro	Pro	Thr		695	700	705

Gln	Ser	Gln	Gln	Thr	Gln	Pro	Pro	Val	Ala	Pro	Gln	Ala	Pro	Ser	710	715	720
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 His Arg Lys Tyr Trp Cys Arg Lys Gly Gly Ile Leu Phe Ser Arg

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Ser	Leu	Phe	Val	Phe	Pro	Gly	Pro	Cys	Cys	Pro	Pro	Ser	Pro	Ser	
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Pro	Thr	Phe	Gln	Pro	Leu	Ala	Thr	Thr	Arg	Leu	Gln	Pro	Lys	Ala	
				140					145					150	
Lys	Ala	Gln	Gln	Thr	Gln	Pro	Pro	Gly	Leu	Thr	Ser	Pro	Gly	Leu	
				155					160					165	
Tyr	Pro	Ala	Ala	Thr	Thr	Ala	Lys	Gln	Gly	Lys	Thr	Gly	Ala	Glu	
				170					175					180	
Ala	Pro	Pro	Leu	Pro	Gly	Thr	Ser	Gln	Tyr	Gly	His	Glu	Arg	Thr	
				185					190					195	
Ser	Gln	Tyr	Thr	Gly	Thr	Ser	Pro	His	Pro	Ala	Thr	Ser	Pro	Pro	
				200					205					210	
Ala	Gly	Ser	Ser	Arg	Pro	Pro	Met	Gln	Leu	Asp	Ser	Thr	Ser	Ala	
				215					220					225	
Glu	Asp	Thr	Ser	Pro	Ala	Leu	Ser	Ser	Gly	Ser	Ser	Lys	Pro	Arg	
				230					235					240	
Val	Ser	Ile	Pro	Met	Val	Arg	Ile	Leu	Ala	Pro	Val	Leu	Val	Leu	
				245					250					255	
Leu	Ser	Leu	Leu	Ser	Ala	Ala	Gly	Leu	Ile	Ala	Phe	Cys	Ser	His	
				260					265					270	
Leu	Leu	Leu	Trp	Arg	Lys	Glu	Ala	Gln	Gln	Ala	Thr	Glu	Thr	Gln	
				275					280					285	
Arg	Asn	Glu	Lys	Phe	Trp	Leu	Ser	Arg	Leu	Thr	Ala	Glu	Glu	Lys	
				290					295					300	
Glu	Ala	Pro	Ser	Gln	Ala	Pro	Glu	Gly	Asp	Val	Ile	Ser	Met	Pro	
				305					310					315	
Pro	Leu	His	Thr	Ser	Glu	Glu	Glu	Leu	Gly	Phe	Ser	Lys	Phe	Val	
				320					325					330	

Ser Ala

<210> 217  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 217  
ccctgcagtg cacctacagg gaag 24

<210> 218  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 218  
ctgtcttccc ctgcttggt gtgg 24

<210> 219  
<211> 47  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 219  
ggtgcaggaa ggggtgggac ctcttctctc gctgctctgg ccacatc 47

<210> 220  
<211> 950  
<212> DNA  
<213> Homo sapiens

<400> 220  
ttgtgactaa aagctggcct agcaggccag ggagtgcagc tgcaggcgtg 50  
gggggtggcag gagccgcaga gccagagcag acagccgaga aacaggtgga 100  
cagtggtgaaa gaaccagtgg tctcgctctg ttgccaggc tagagtgtac 150  
tggcgtgatc atagctcact gcagcctcag actcctggac ttgagaaatc 200  
ctcctgcctt agcctcctgc atatctggga ctccaggggt gcactcaagc 250  
cctgtttctt ctccttctgt gagtggacca cggaggctgg tgagctgcct 300  
gtcatcccaa agctcagctc tgagccagag tgggtggtggc tccacctctg 350  
ccgccggcat agaagccagg agcagggctc tcagaaggcg gtggtgccca 400



gctgggatca tgttgttggc cctggtctgt ctgctcagct gcctgctacc 450  
ctccagtgag gccaaactct acggtcggtg tgaactggcc agagtgtac 500  
atgacttcgg gctggacgga taccggggat acagcctggc tgactgggtc 550  
tgccttgctt atttcacaag cggtttcaac gcagctgctt tggactacga 600  
ggctgatggg agcaccaaca acgggatctt ccagatcaac agccggaggt 650  
ggtgcagcaa cctcaccocg aacgtcccca acgtgtgccg gatgtactgc 700  
tcagatttgt tgaatcctaa tctcaaggat accgttatct gtgccatgaa 750  
gataacccaa gagcctcagg gtctgggtta ctgggaggcc tggaggcatc 800  
actgccaggg aaaagacctc actgaatggg tggatggctg tgacttctag 850  
gatggacgga accatgcaca gcaggctggg aaatgtggtt tggttcctga 900  
cctagccttg ggaagacaag ccagcgaata aaggatggtt gaacgtgaaa 950

<210> 221  
<211> 146  
<212> PRT  
<213> Homo sapiens

<400> 221  
Met Leu Leu Ala Leu Val Cys Leu Leu Ser Cys Leu Leu Pro Ser  
1 5 10 15  
Ser Glu Ala Lys Leu Tyr Gly Arg Cys Glu Leu Ala Arg Val Leu  
20 25 30  
His Asp Phe Gly Leu Asp Gly Tyr Arg Gly Tyr Ser Leu Ala Asp  
35 40 45  
Trp Val Cys Leu Ala Tyr Phe Thr Ser Gly Phe Asn Ala Ala Ala  
50 55 60  
Leu Asp Tyr Glu Ala Asp Gly Ser Thr Asn Asn Gly Ile Phe Gln  
65 70 75  
Ile Asn Ser Arg Arg Trp Cys Ser Asn Leu Thr Pro Asn Val Pro  
80 85 90  
Asn Val Cys Arg Met Tyr Cys Ser Asp Leu Leu Asn Pro Asn Leu  
95 100 105  
Lys Asp Thr Val Ile Cys Ala Met Lys Ile Thr Gln Glu Pro Gln  
110 115 120  
Gly Leu Gly Tyr Trp Glu Ala Trp Arg His His Cys Gln Gly Lys  
125 130 135  
Asp Leu Thr Glu Trp Val Asp Gly Cys Asp Phe  
140 145

<210> 222  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 222  
gggatcatgt tgttggccct ggtc 24

<210> 223  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 223  
gcaaggcaga ccagtcagc cag 23

<210> 224  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 224  
ctgcctgcta ccctccaagt gaggccaagc tctacggtcg ttgtg 45

<210> 225  
<211> 2049  
<212> DNA  
<213> Homo sapiens

<400> 225  
agccgctgcc ccgggccggg cgcccgcggc ggcacccatga gtccccgctc 50  
gtgcctgcgt tcgctgcgcc tctctgtctt cgcggtcttc tcagccgccg 100  
cgagcaactg gctgtacctg gccaaagctgt cgtcgggtggg gagcatctca 150  
gaggaggaga cgtgcgagaa actcaagggc ctgatccaga ggcaggtgca 200  
gatgtgcaag cggaacctgg aagtcattga ctcggtgcgc cgcggtgccc 250  
agctggccat tgaggagtgc cagtaccagt tccggaaccg gcgctggaac 300  
tgctccacac tcgactcctt gcccgctctt ggcaagggtg tgacgcaagg 350  
gactcgggag gcggccttcg tgtacgcat ctcttcggca ggtgtggcct 400  
ttgcagtgac gcgggcgtgc agcagtgggg agctggagaa gtgcggctgt 450

gacaggacag tgcattgggt cagcccacag ggcttccagt ggtcaggatg 500  
ctctgacaac atcgccctacg gtgtggcctt ctacacagtcg tttgtggatg 550  
tgcgggagag aagcaagggg gcctcgcca gcagagccct catgaacctc 600  
cacaacaatg aggcggcag gaaggccatc ctgacacaca tgcgggtgga 650  
atgcaagtgc cacgggggtg caggctcctg tgaggtaaag acgtgctggc 700  
gagccgtgcc gcccttccgc cagggtgggc acgcactgaa ggagaagttt 750  
gatggtgcca ctgagggtga gccacgccc gtgggctcct ccagggcact 800  
ggtaccacgc aacgcacagt tcaagccgca cacagatgag gacctggtgt 850  
acttgagacc tagccccgac ttctgtgagc aggacatgcg cagcggcgtg 900  
ctgggcacga gggccgcac atgcaacaag acgtccaagg ccatcgacgg 950  
ctgtgagctg ctgtgctgtg gccgcggctt ccacacggcg cagggtggagc 1000  
tggtgaacg ctgcagctgc aaattccact ggtgctgctt cgtcaagtgc 1050  
cggcagtgcc agcggctcgt ggagttgcac acgtgccgat gaccgcctgc 1100  
ctagccctgc gccggcaacc acctagtggc ccagggaagg ccgataattt 1150  
aaacagtctc ccaccaccta cccaagaga tactggttgt attttttgtt 1200  
ctggttttgt ttttgggtcc tcatgttatt tattgccga accaggcagg 1250  
caacccaag ggcaccaacc agggcctccc caaagcctgg gcctttgtgg 1300  
ctgccactga ccaaaggac cttgctcgtg ccgctggctg cccgcatgtg 1350  
gctgccactg accactcagt tgttatctgt gtccgttttt ctacttgcag 1400  
acctaaggty gagtaacaag gagtattacc accacatggc tactgaccgt 1450  
gtcatcgggg aagagggggc cttatggcag ggaaaatagg taccgacttg 1500  
atggaagtca caccctctgg aaaaaagaac tcttaactct ccagcacaca 1550  
tacacatgga ctctggcag cttgagccta gaagccatgt ctctcaaatg 1600  
ccctgagaaa gggaacaagc agataccagg tcaagggcac caggttcatt 1650  
tcagccctta catggacagc tagaggttcg atatctgtgg gtccttccag 1700  
gcaagaagag ggagatgaga gcaagagacg actgaagtcc caccctagaa 1750  
cccagcctgc cccagcctgc ccctgggaag aggaaactta accactcccc 1800  
agacccacct aggcaggcat ataggctgcc atcctggacc agggatcccg 1850

gctgtgcctt tgcagtcatg cccgagtcac ctttcacagc gctgttcctc 1900  
catgaaactg aaaaacacac acacacacac acacacacac acacacacac 1950  
acacacacac ggacacacac acacacctgc gagagagagg gaggaaaggg 2000  
ctgtgccttt gcagtcatgc ccgagtcacc tttcacagca ctgttcctc 2049

<210> 226  
<211> 351  
<212> PRT  
<213> Homo sapiens

<400> 226  
Met Ser Pro Arg Ser Cys Leu Arg Ser Leu Arg Leu Leu Val Phe  
1 5 10 15  
Ala Val Phe Ser Ala Ala Ala Ser Asn Trp Leu Tyr Leu Ala Lys  
20 25 30  
Leu Ser Ser Val Gly Ser Ile Ser Glu Glu Glu Thr Cys Glu Lys  
35 40 45  
Leu Lys Gly Leu Ile Gln Arg Gln Val Gln Met Cys Lys Arg Asn  
50 55 60  
Leu Glu Val Met Asp Ser Val Arg Arg Gly Ala Gln Leu Ala Ile  
65 70 75  
Glu Glu Cys Gln Tyr Gln Phe Arg Asn Arg Arg Trp Asn Cys Ser  
80 85 90  
Thr Leu Asp Ser Leu Pro Val Phe Gly Lys Val Val Thr Gln Gly  
95 100 105  
Thr Arg Glu Ala Ala Phe Val Tyr Ala Ile Ser Ser Ala Gly Val  
110 115 120  
Ala Phe Ala Val Thr Arg Ala Cys Ser Ser Gly Glu Leu Glu Lys  
125 130 135  
Cys Gly Cys Asp Arg Thr Val His Gly Val Ser Pro Gln Gly Phe  
140 145 150  
Gln Trp Ser Gly Cys Ser Asp Asn Ile Ala Tyr Gly Val Ala Phe  
155 160 165  
Ser Gln Ser Phe Val Asp Val Arg Glu Arg Ser Lys Gly Ala Ser  
170 175 180  
Ser Ser Arg Ala Leu Met Asn Leu His Asn Asn Glu Ala Gly Arg  
185 190 195  
Lys Ala Ile Leu Thr His Met Arg Val Glu Cys Lys Cys His Gly  
200 205 210  
Val Ser Gly Ser Cys Glu Val Lys Thr Cys Trp Arg Ala Val Pro

215										220				225			
Pro	Phe	Arg	Gln	Val	Gly	His	Ala	Leu	Lys	Glu	Lys	Phe	Asp	Gly			
230										235				240			
Ala	Thr	Glu	Val	Glu	Pro	Arg	Arg	Val	Gly	Ser	Ser	Arg	Ala	Leu			
245										250				255			
Val	Pro	Arg	Asn	Ala	Gln	Phe	Lys	Pro	His	Thr	Asp	Glu	Asp	Leu			
260										265				270			
Val	Tyr	Leu	Glu	Pro	Ser	Pro	Asp	Phe	Cys	Glu	Gln	Asp	Met	Arg			
275										280				285			
Ser	Gly	Val	Leu	Gly	Thr	Arg	Gly	Arg	Thr	Cys	Asn	Lys	Thr	Ser			
290										295				300			
Lys	Ala	Ile	Asp	Gly	Cys	Glu	Leu	Leu	Cys	Cys	Gly	Arg	Gly	Phe			
305										310				315			
His	Thr	Ala	Gln	Val	Glu	Leu	Ala	Glu	Arg	Cys	Ser	Cys	Lys	Phe			
320										325				330			
His	Trp	Cys	Cys	Phe	Val	Lys	Cys	Arg	Gln	Cys	Gln	Arg	Leu	Val			
335										340				345			
Glu	Leu	His	Thr	Cys	Arg												
350																	

<210> 227

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 227

gctgcagctg caaattccac tgg 23

<210> 228

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 228

tggtgggaga ctgtttaaat tatcggcc 28

<210> 229

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 229

tgcttcgtca agtgccggca gtgccagcgg ctctggagt t 41

<210> 230

<211> 1355

<212> DNA

<213> Homo sapiens

<400> 230

cggacgcgtg ggcggacgcg tgggcggacg cgtgggcgga cgcgtgggct 50  
gggtgcctgc atcgccatgg acaccaccag gtacagcaag tggggcggca 100  
gctccgagga ggtccccgga gggccctggg gacgctgggt gactggagc 150  
aggagacccc tcttcttggc cctggctgtc ctggtcacca cagtcctttg 200  
ggctgtgatt ctgagtatcc tattgtccaa ggcctccacg gagcgcgcgg 250  
cgctgcttga cggccacgac ctgctgagga caaacgcctc gaagcagacg 300  
gcggcgctgg gtgccctgaa ggaggaggtc ggagactgcc acagctgctg 350  
ctcggggacg caggcgcagc tgcagaccac gcgcgcggag cttggggagg 400  
cgcaggcgaa gctgatggag caggagagcg ccctgcggga actgcgtgag 450  
cgcgtgaccc agggcttggc tgaagccggc aggggcccgtg aggacgtccg 500  
cactgagctg ttccggggcg tggaggccgt gaggctccag aacaactcct 550  
gcgagccgtg ccccacgtcg tggtgtcct tcgagggctc ctgctacttt 600  
ttctctgtgc caaagacgac gtgggcggcg gcgcaggatc actgcgcaga 650  
tgccagcgcg cacctggtga tcgttggggg cctggatgag cagggcttcc 700  
tcactcgaa cacgcgtggc cgtgggttact ggctgggcct gagggtgtg 750  
cgccatctgg gcaaggttca gggctaccag tgggtggacg gagtctctct 800  
cagcttcagc cactggaacc agggagagcc caatgacgct tgggggcgcg 850  
agaactgtgt catgatgctg cacacggggc tgtggaacga cgcaccgtgt 900  
gacagcgaga aggacggctg gatctgtgag aaaaggcaca actgctgacc 950  
ccgccagtg ccctggagcc gcgccattg cagcatgtcg tatcctgggg 1000  
gctgctcacc tccctggctc ctggagctga ttgccaaaga gtttttttct 1050  
tctcatcca ccgctgctga gtctcagaaa cacttgcccc aacatagccc 1100  
tgtccagccc agtgccctgg ctctgggacc tccatgccga cctcatccta 1150

actccactca cgcagaccca acctaacctc cactagctcc aaaatccctg 1200  
ctcctgcgctc cccgtgatat gcctccactt ctctccctaa ccaaggttag 1250  
gtgactgagg actggagctg tttggttttc tcgcattttc caccaaactg 1300  
gaagctgttt ttgcagcctg aggaagcatc aataaatatt tgagaaatga 1350  
aaaaa 1355

<210> 231  
<211> 293  
<212> PRT  
<213> Homo sapiens

<400> 231  
Met Asp Thr Thr Arg Tyr Ser Lys Trp Gly Gly Ser Ser Glu Glu  
1 5 10 15  
Val Pro Gly Gly Pro Trp Gly Arg Trp Val His Trp Ser Arg Arg  
20 25 30  
Pro Leu Phe Leu Ala Leu Ala Val Leu Val Thr Thr Val Leu Trp  
35 40 45  
Ala Val Ile Leu Ser Ile Leu Leu Ser Lys Ala Ser Thr Glu Arg  
50 55 60  
Ala Ala Leu Leu Asp Gly His Asp Leu Leu Arg Thr Asn Ala Ser  
65 70 75  
Lys Gln Thr Ala Ala Leu Gly Ala Leu Lys Glu Glu Val Gly Asp  
80 85 90  
Cys His Ser Cys Cys Ser Gly Thr Gln Ala Gln Leu Gln Thr Thr  
95 100 105  
Arg Ala Glu Leu Gly Glu Ala Gln Ala Lys Leu Met Glu Gln Glu  
110 115 120  
Ser Ala Leu Arg Glu Leu Arg Glu Arg Val Thr Gln Gly Leu Ala  
125 130 135  
Glu Ala Gly Arg Gly Arg Glu Asp Val Arg Thr Glu Leu Phe Arg  
140 145 150  
Ala Leu Glu Ala Val Arg Leu Gln Asn Asn Ser Cys Glu Pro Cys  
155 160 165  
Pro Thr Ser Trp Leu Ser Phe Glu Gly Ser Cys Tyr Phe Phe Ser  
170 175 180  
Val Pro Lys Thr Thr Trp Ala Ala Ala Gln Asp His Cys Ala Asp  
185 190 195  
Ala Ser Ala His Leu Val Ile Val Gly Gly Leu Asp Glu Gln Gly  
200 205 210

Phe	Leu	Thr	Arg	Asn	Thr	Arg	Gly	Arg	Gly	Tyr	Trp	Leu	Gly	Leu
				215					220					225
Arg	Ala	Val	Arg	His	Leu	Gly	Lys	Val	Gln	Gly	Tyr	Gln	Trp	Val
				230					235					240
Asp	Gly	Val	Ser	Leu	Ser	Phe	Ser	His	Trp	Asn	Gln	Gly	Glu	Pro
				245					250					255
Asn	Asp	Ala	Trp	Gly	Arg	Glu	Asn	Cys	Val	Met	Met	Leu	His	Thr
				260					265					270
Gly	Leu	Trp	Asn	Asp	Ala	Pro	Cys	Asp	Ser	Glu	Lys	Asp	Gly	Trp
				275					280					285
Ile	Cys	Glu	Lys	Arg	His	Asn	Cys							
				290										

<210> 232  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 232  
 gcgagaactg tgtcatgatg ctgc 24

<210> 233  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 233  
 gtttctgaga ctcagcagcg gtgg 24

<210> 234  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 234  
 caccgtgtga cagcgagaag gacggctgga tctgtgagaa aaggcacaac 50

<210> 235  
 <211> 1847  
 <212> DNA  
 <213> Homo sapiens



<400> 235

gccaggggaa gagggatgac cgacccgggg aagggtcgctg ggcagggcga 50  
gttgggaaag cggcagcccc cgccgcccc gcagcccctt ctctctcttt 100  
ctcccacgtc ctatctgcct ctcgctggag gccaggccgt gcagcatcga 150  
agacaggagg aactggagcc tcattggccg gcccggggcg ccggcctcgg 200  
gcttaaataag gagctccggg ctctggctgg gacccgaccg ctgccggccg 250  
cgctcccgt gctcctgccg ggtgatggaa aaccccagcc cggccgccgc 300  
cctgggcaag gccctctgcg ctctcctcct ggccactctc ggcgccgccg 350  
gccagcctct tgggggagag tccatctgtt ccgccagagc cccggccaaa 400  
tacagcatca ccttcacggg caagtggagc cagacggcct tccccaagca 450  
gtaccccctg ttccgc'cccc ctgcgcagtg gtcttcgctg ctggggggccg 500  
cgcatagctc cgactacagc atgtggagga agaaccagta cgtcagtaac 550  
gggctgcgcg actttgcgga gcgcggcgag gcctgggcgc tgatgaagga 600  
gatcagaggc gcgggggagg cgctgcagag cgtgcacgag gtgttttcgg 650  
cgcccgccgt cccagcggc accgggcaga cgtcggcgga gctggaggtg 700  
cagcgcaggc actcgctggt ctcgtttgtg gtgcgcatcg tgcccagccc 750  
cgactggttc gtgggcgtgg acagcctgga cctgtgcgac ggggaccgtt 800  
ggcgggaaca ggcggcgctg gacctgtacc cctacgacgc cgggacggac 850  
agcggcttca ctttctctc ccccaacttc gccaccatcc cgcaggacac 900  
ggtgaccgag ataacgtcct cctctcccag ccacccggcc aactccttct 950  
actaccgcg gctgaaggcc ctgcctcca tcgccagggt gacactgctg 1000  
cggctgcgac agagccccag ggccttcato cctcccgcc cagtccctgcc 1050  
cagcagggac aatgagattg tagacagcgc ctcagttcca gaaacgccgc 1100  
tggactgcga ggtctccctg tggtcgtcct ggggactgtg cggaggccac 1150  
tgtgggaggc tcgggaccaa gagcaggact cgctacgtcc ggggccagcc 1200  
cgccaacaac gggagcccct gccccgagct cgaagaagag gctgagtgcg 1250  
tccctgataa ctgcgtctaa gaccagagcc ccgcagcccc tggggcccc 1300  
cggagccatg ggggtgtcggg ggctcctgtg caggctcatg ctgcaggcgg 1350  
ccgagggcac agggggtttc gcgctgctcc tgaccgcggt gaggccgcgc 1400

cgaccatctc tgcactgaag ggccctctgg tggccggcac gggcattggg 1450  
 aaacagcctc ctcctttccc aaccttgctt cttagggggcc cccgtgtccc 1500  
 gtctgtcttc agcctcctcc tcctgcagga taaagtcac cccaaggctc 1550  
 cagctactct aaattatgtc tccttataag ttattgctgc tccaggagat 1600  
 tgtccttcat cgtccagggg cctggctccc acgtggttgc agatacctca 1650  
 gacctggtgc tctaggctgt gctgagccca ctctcccgag ggcgcatcca 1700  
 agcggggggc acttgagaag tgaataaatg gggcggtttc ggaagcgtca 1750  
 gtgtttccat gttatggatc tctctgcgtt tgaataaaga ctatctctgt 1800  
 tgctcacaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 1847

<210> 236  
 <211> 331  
 <212> PRT  
 <213> Homo sapiens

<400> 236  
 Met Glu Asn Pro Ser Pro Ala Ala Ala Leu Gly Lys Ala Leu Cys  
     1                    5                    10                    15  
 Ala Leu Leu Leu Ala Thr Leu Gly Ala Ala Gly Gln Pro Leu Gly  
                     20                    25                    30  
 Gly Glu Ser Ile Cys Ser Ala Arg Ala Pro Ala Lys Tyr Ser Ile  
                     35                    40                    45  
 Thr Phe Thr Gly Lys Trp Ser Gln Thr Ala Phe Pro Lys Gln Tyr  
                     50                    55                    60  
 Pro Leu Phe Arg Pro Pro Ala Gln Trp Ser Ser Leu Leu Gly Ala  
                     65                    70                    75  
 Ala His Ser Ser Asp Tyr Ser Met Trp Arg Lys Asn Gln Tyr Val  
                     80                    85                    90  
 Ser Asn Gly Leu Arg Asp Phe Ala Glu Arg Gly Glu Ala Trp Ala  
                     95                    100                    105  
 Leu Met Lys Glu Ile Glu Ala Ala Gly Glu Ala Leu Gln Ser Val  
                     110                    115                    120  
 His Glu Val Phe Ser Ala Pro Ala Val Pro Ser Gly Thr Gly Gln  
                     125                    130                    135  
 Thr Ser Ala Glu Leu Glu Val Gln Arg Arg His Ser Leu Val Ser  
                     140                    145                    150  
 Phe Val Val Arg Ile Val Pro Ser Pro Asp Trp Phe Val Gly Val  
                     155                    160                    165

Asp Ser Leu Asp	Leu Cys Asp Gly Asp	Arg Trp Arg Glu Gln Ala	170	175	180
Ala Leu Asp Leu	Tyr Pro Tyr Asp Ala Gly Thr Asp Ser Gly Phe		185	190	195
Thr Phe Ser Ser	Pro Asn Phe Ala Thr Ile Pro Gln Asp Thr Val		200	205	210
Thr Glu Ile Thr	Ser Ser Ser Pro Ser His Pro Ala Asn Ser Phe		215	220	225
Tyr Tyr Pro Arg	Leu Lys Ala Leu Pro Pro Ile Ala Arg Val Thr		230	235	240
Leu Leu Arg Leu	Arg Gln Ser Pro Arg Ala Phe Ile Pro Pro Ala		245	250	255
Pro Val Leu Pro	Ser Arg Asp Asn Glu Ile Val Asp Ser Ala Ser		260	265	270
Val Pro Glu Thr	Pro Leu Asp Cys Glu Val Ser Leu Trp Ser Ser		275	280	285
Trp Gly Leu Cys	Gly Gly His Cys Gly Arg Leu Gly Thr Lys Ser		290	295	300
Arg Thr Arg Tyr	Val Arg Val Gln Pro Ala Asn Asn Gly Ser Pro		305	310	315
Cys Pro Glu Leu	Glu Glu Glu Ala Glu Cys Val Pro Asp Asn Cys		320	325	330

Val

<210> 237

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 237

cagcactgcc aggggaagag gg 22

<210> 238

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 238

caggactcgc tacgtccg 18

<210> 239  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 239  
cagccccttc tcctcctttc tccc 24

<210> 240  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 240  
gcagttatca gggacgcact cagcc 25

<210> 241  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 241  
ccagcgagag gcagatag 18

<210> 242  
<211> 23  
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<400> 242  
cggtcaccgt gtctgcggg atg 23

<210> 243  
<211> 42  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 243  
cagccccttc tcctcctttc tcccacgtcc tatctgcctc tc 42

<210> 244

<211> 1894  
<212> DNA  
<213> Homo sapiens

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aggaagagtg tactcgtagg cggacagctt tagtggccgg ccggccgctc 150  
tcacccccg taaggagcag agtcctttgt actgaccaag atgagcaaca 200  
tctacatcca ggagcctccc acgaatggga aggtttttatt gaaaactaca 250  
gctggagata ttgacataga gttgtgggtcc aaagaagctc ctaaagcttg 300  
cagaaatfff atccaactff gtttggaagc ttattatgac aataccatff 350  
ttcatagagt tgtgcctggt ttcatagtcc aaggcggaga tcctactggc 400  
acagggagtg gtggagagtc tatctatgga gcgccattca aagatgaatt 450  
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<210> 245
<211> 472
<212> PRT
<213> Homo sapiens

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Leu Leu Lys Thr Thr Ala Gly Asp Ile Asp Ile Glu Leu Trp Ser
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Lys Glu Ala Pro Lys Ala Cys Arg Asn Phe Ile Gln Leu Cys Leu
          35              40              45

Glu Ala Tyr Tyr Asp Asn Thr Ile Phe His Arg Val Val Pro Gly
          50              55              60

Phe Ile Val Gln Gly Gly Asp Pro Thr Gly Thr Gly Ser Gly Gly
          65              70              75

Glu Ser Ile Tyr Gly Ala Pro Phe Lys Asp Glu Phe His Ser Arg
          80              85              90

Leu Arg Phe Asn Arg Arg Gly Leu Val Ala Met Ala Asn Ala Gly
          95              100             105

Ser His Asp Asn Gly Ser Gln Phe Phe Phe Thr Leu Gly Arg Ala
          110             115             120

Asp Glu Leu Asn Asn Lys His Thr Ile Phe Gly Lys Val Thr Gly
          125             130             135

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Asp Thr Val Tyr	Asn Met Leu Arg Leu	Ser Glu Val Asp Ile	Asp
	140	145	150
Asp Asp Glu Arg	Pro His Asn Pro His	Lys Ile Lys Ser Cys	Glu
	155	160	165
Val Leu Phe Asn	Pro Phe Asp Asp Ile	Ile Pro Arg Glu Ile	Lys
	170	175	180
Arg Leu Lys Lys	Glu Lys Pro Glu Glu	Glu Val Lys Lys Leu	Lys
	185	190	195
Pro Lys Gly Thr	Lys Asn Phe Ser Leu	Leu Ser Phe Gly Glu	Glu
	200	205	210
Ala Glu Glu Glu	Glu Glu Glu Val Asn	Arg Val Ser Gln Ser	Met
	215	220	225
Lys Gly Lys Ser	Lys Ser Ser His Asp	Leu Leu Lys Asp Asp	Pro
	230	235	240
His Leu Ser Ser	Val Pro Val Val Glu	Ser Glu Lys Gly Asp	Ala
	245	250	255
Pro Asp Leu Val	Asp Asp Gly Glu Asp	Glu Ser Ala Glu His	Asp
	260	265	270
Glu Tyr Ile Asp	Gly Asp Glu Lys Asn	Leu Met Arg Glu Arg	Ile
	275	280	285
Ala Lys Lys Leu	Lys Lys Asp Thr Ser	Ala Asn Val Lys Ser	Ala
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Gly Glu Gly Glu	Val Glu Lys Lys Ser	Val Ser Arg Ser Glu	Glu
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Leu Arg Lys Glu	Ala Arg Gln Leu Lys	Arg Glu Leu Leu Ala	Ala
	320	325	330
Lys Gln Lys Lys	Val Glu Asn Ala Ala	Lys Gln Ala Glu Lys	Arg
	335	340	345
Ser Glu Glu Glu	Glu Ala Pro Pro Asp	Gly Ala Val Ala Glu	Tyr
	350	355	360
Arg Arg Glu Lys	Gln Lys Tyr Glu Ala	Leu Arg Lys Gln Gln	Ser
	365	370	375
Lys Lys Gly Thr	Ser Arg Glu Asp Gln	Thr Leu Ala Leu Leu	Asn
	380	385	390
Gln Phe Lys Ser	Lys Leu Thr Gln Ala	Ile Ala Glu Thr Pro	Glu
	395	400	405
Asn Asp Ile Pro	Glu Thr Glu Val Glu	Asp Asp Glu Gly Trp	Met
	410	415	420

Ser His Val Leu Gln Phe Glu Asp Lys Ser Arg Lys Val Lys Asp  
425 430 435

Ala Ser Met Gln Asp Ser Asp Thr Phe Glu Ile Tyr Asp Pro Arg  
440 445 450

Asn Pro Val Asn Lys Arg Arg Arg Glu Glu Ser Lys Lys Leu Met  
455 460 465

Arg Glu Lys Lys Glu Arg Arg  
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<210> 246

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 246

tgcgagatc ctactggcac aggg 24

<210> 247

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 247

cgagttagtc agagcatg 18

<210> 248

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 248

cagatggtgc tggtgccg 18

<210> 249

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 249

caactggaac aggaactgag atgtggatc 29

<210> 250



<211> 24  
<212> DNA  
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<220>  
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<400> 250  
ctggttcagc agtgcaaggg tctg 24

<210> 251  
<211> 18  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 251  
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<210> 252  
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<212> DNA  
<213> Artificial Sequence

<220>  
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<210> 253  
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<213> Homo sapiens

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<210> 254  
 <211> 545  
 <212> PRT  
 <213> Homo sapiens

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 35 40 45  
 Asn Leu Gly Ser Thr Ser Thr Pro Ala Thr Thr Ser Ala Pro Ser  
 50 55 60  
 Ser Gly Phe Gly Thr Gly Leu Phe Gly Ser Lys Pro Ala Thr Gly  
 65 70 75  
 Phe Thr Leu Gly Gly Thr Asn Thr Gly Ala Leu His Thr Lys Arg  
 80 85 90  
 Pro Gln Val Val Thr Lys Tyr Gly Thr Leu Gln Gly Lys Gln Met  
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 His Val Gly Lys Thr Pro Ile Gln Val Phe Leu Gly Val Pro Phe  
 110 115 120  
 Ser Arg Pro Pro Leu Gly Ile Leu Arg Phe Ala Pro Pro Glu Pro  
 125 130 135

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Gly	Trp	Ser	Leu	Ala	Leu	Ser	Pro	Gly	Trp	Ser	Ala	Val	Ala	Arg	155	160	165
Ser	Arg	Leu	Thr	Ala	Thr	Ser	Ala	Ser	Arg	Val	Gln	Ala	Ser	Leu	170	175	180
Leu	Pro	Gln	Pro	Leu	Ser	Val	Trp	Gly	Tyr	Arg	Cys	Leu	Gln	Glu	185	190	195
Ser	Trp	Gly	Gln	Leu	Ala	Ser	Met	Tyr	Val	Ser	Thr	Arg	Glu	Arg	200	205	210
Tyr	Lys	Trp	Leu	Arg	Phe	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Val	215	220	225
Tyr	Ala	Pro	Ala	Arg	Ala	Pro	Gly	Asp	Pro	Gln	Leu	Pro	Val	Met	230	235	240
Val	Trp	Phe	Pro	Gly	Gly	Ala	Phe	Ile	Val	Gly	Ala	Ala	Ser	Ser	245	250	255
Tyr	Glu	Gly	Ser	Asp	Leu	Ala	Ala	Arg	Glu	Lys	Val	Val	Leu	Val	260	265	270
Phe	Leu	Gln	His	Arg	Leu	Gly	Ile	Phe	Gly	Phe	Leu	Ser	Thr	Asp	275	280	285
Asp	Ser	His	Ala	Arg	Gly	Asn	Trp	Gly	Leu	Leu	Asp	Gln	Met	Ala	290	295	300
Ala	Leu	Arg	Trp	Val	Gln	Glu	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asp	305	310	315
Pro	Gly	Asn	Val	Thr	Leu	Phe	Gly	Gln	Ser	Ala	Gly	Ala	Met	Ser	320	325	330
Ile	Ser	Gly	Leu	Met	Met	Ser	Pro	Leu	Ala	Ser	Gly	Leu	Phe	His	335	340	345
Arg	Ala	Ile	Ser	Gln	Ser	Gly	Thr	Ala	Leu	Phe	Arg	Leu	Phe	Ile	350	355	360
Thr	Ser	Asn	Pro	Leu	Lys	Val	Ala	Lys	Lys	Val	Ala	His	Leu	Ala	365	370	375
Gly	Cys	Asn	His	Asn	Ser	Thr	Gln	Ile	Leu	Val	Asn	Cys	Leu	Arg	380	385	390
Ala	Leu	Ser	Gly	Thr	Lys	Val	Met	Arg	Val	Ser	Asn	Lys	Met	Arg	395	400	405
Phe	Leu	Gln	Leu	Asn	Phe	Gln	Arg	Asp	Pro	Glu	Glu	Ile	Ile	Trp	410	415	420

Ser	Met	Ser	Pro	Val	Val	Asp	Gly	Val	Val	Ile	Pro	Asp	Asp	Pro	425	430	435
Leu	Val	Leu	Leu	Thr	Gln	Gly	Lys	Val	Ser	Ser	Val	Pro	Tyr	Leu	440	445	450
Leu	Gly	Val	Asn	Asn	Leu	Glu	Phe	Asn	Trp	Leu	Leu	Pro	Tyr	Asn	455	460	465
Ile	Thr	Lys	Glu	Gln	Val	Pro	Leu	Val	Val	Glu	Glu	Tyr	Leu	Asp	470	475	480
Asn	Val	Asn	Glu	His	Asp	Trp	Lys	Met	Leu	Arg	Asn	Arg	Met	Met	485	490	495
Asp	Ile	Val	Gln	Asp	Ala	Thr	Phe	Val	Tyr	Ala	Thr	Leu	Gln	Thr	500	505	510
Ala	His	Tyr	His	Arg	Glu	Thr	Pro	Met	Met	Gly	Ile	Cys	Pro	Ala	515	520	525
Gly	His	Ala	Thr	Thr	Arg	Met	Lys	Ser	Thr	Cys	Ser	Trp	Ile	Leu	530	535	540
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 <223> Synthetic oligonucleotide probe

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<210> 256  
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<220>  
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<400> 256  
 ccacctcagg aagccgaaga tgcc 24

<210> 257  
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<400> 257

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<210> 258

<211> 2764

<212> DNA

<213> Homo sapiens

<400> 258

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<210> 259  
 <211> 544  
 <212> PRT  
 <213> Homo sapiens

<400> 259  
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 Val Pro Glu Gly Leu Cys Ile Ser Val Pro Cys Ser Phe Ser Tyr  
 35 40 45  
 Pro Arg Gln Asp Trp Thr Gly Ser Thr Pro Ala Tyr Gly Tyr Trp  
 50 55 60  
 Phe Lys Ala Val Thr Glu Thr Thr Lys Gly Ala Pro Val Ala Thr  
 65 70 75  
 Asn His Gln Ser Arg Glu Val Glu Met Ser Thr Arg Gly Arg Phe  
 80 85 90  
 Gln Leu Thr Gly Asp Pro Ala Lys Gly Asn Cys Ser Leu Val Ile  
 95 100 105  
 Arg Asp Ala Gln Met Gln Asp Glu Ser Gln Tyr Phe Phe Arg Val  
 110 115 120  
 Glu Arg Gly Ser Tyr Val Thr Tyr Asn Phe Met Asn Asp Gly Phe  
 125 130 135  
 Phe Leu Lys Val Thr Val Leu Ser Phe Thr Pro Arg Pro Gln Asp  
 140 145 150  
 His Asn Thr Asp Leu Thr Cys His Val Asp Phe Ser Arg Lys Gly  
 155 160 165  
 Val Ser Ala Gln Arg Thr Val Arg Leu Arg Val Ala Tyr Ala Pro  
 170 175 180  
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 185 190 195  
 Glu Pro Gln Pro Gln Gly Asn Val Pro Tyr Leu Glu Ala Gln Lys  
 200 205 210  
 Gly Gln Phe Leu Arg Leu Leu Cys Ala Ala Asp Ser Gln Pro Pro  
 215 220 225



Ala Thr Leu Ser	Trp Val Leu Gln Asn	Arg Val Leu Ser Ser	Ser
	230	235	240
His Pro Trp Gly	Pro Arg Pro Leu Gly	Leu Glu Leu Pro Gly	Val
	245	250	255
Lys Ala Gly Asp	Ser Gly Arg Tyr Thr	Cys Arg Ala Glu Asn	Arg
	260	265	270
Leu Gly Ser Gln	Gln Arg Ala Leu Asp	Leu Ser Val Gln Tyr	Pro
	275	280	285
Pro Glu Asn Leu	Arg Val Met Val Ser	Gln Ala Asn Arg Thr	Val
	290	295	300
Leu Glu Asn Leu	Gly Asn Gly Thr Ser	Leu Pro Val Leu Glu	Gly
	305	310	315
Gln Ser Leu Cys	Leu Val Cys Val Thr	His Ser Ser Pro Pro	Ala
	320	325	330
Arg Leu Ser Trp	Thr Gln Arg Gly Gln	Val Leu Ser Pro Ser	Gln
	335	340	345
Pro Ser Asp Pro	Gly Val Leu Glu Leu	Pro Arg Val Gln Val	Glu
	350	355	360
His Glu Gly Glu	Phe Thr Cys His Ala	Arg His Pro Leu Gly	Ser
	365	370	375
Gln His Val Ser	Leu Ser Leu Ser Val	His Tyr Lys Lys Gly	Leu
	380	385	390
Ile Ser Thr Ala	Phe Ser Asn Gly Ala	Phe Leu Gly Ile Gly	Ile
	395	400	405
Thr Ala Leu Leu	Phe Leu Cys Leu Ala	Leu Ile Ile Met Lys	Ile
	410	415	420
Leu Pro Lys Arg	Arg Thr Gln Thr Glu	Thr Pro Arg Pro Arg	Phe
	425	430	435
Ser Arg His Ser	Thr Ile Leu Asp Tyr	Ile Asn Val Val Pro	Thr
	440	445	450
Ala Gly Pro Leu	Ala Gln Lys Arg Asn	Gln Lys Ala Thr Pro	Asn
	455	460	465
Ser Pro Arg Thr	Pro Pro Pro Pro Gly	Ala Pro Ser Pro Glu	Ser
	470	475	480
Lys Lys Asn Gln	Lys Lys Gln Tyr Gln	Leu Pro Ser Phe Pro	Glu
	485	490	495
Pro Lys Ser Ser	Thr Gln Ala Pro Glu	Ser Gln Glu Ser Gln	Glu
	500	505	510

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Val Lys Phe Gln

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<220>

<223> Synthetic oligonucleotide probe

<400> 260

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<210> 261

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 261

ttctggagcc cagaggggtgc tgag 24

<210> 262

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 262

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<211> 2857

<212> DNA

<213> Homo sapiens

<400> 263

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caacagaaaa ctctcaaaca aagaaagtca agcagccagt gcgatctcat 150

ttgagagtga agcgtggctg ggtgtggaac caattttttg taccagagga 200

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atggaaacaa ttctttccag tacaagcttt tgggagctgg agctggaagt 300  
acttttatca ttgatgaaag aacagggtgac atatatgcca tacagaagct 350  
tgatagagag gagcgatccc tctacatctt aagagcccag gtaatagaca 400  
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<210> 264

<211> 772

<212> PRT

<213> Homo sapiens

<400> 264

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Leu	Trp	Pro	Cys	Leu	Gly	Ala	Thr	Glu	Asn	Ser	Gln	Thr	Lys	Lys	20	25	30	
Val	Lys	Gln	Pro	Val	Arg	Ser	His	Leu	Arg	Val	Lys	Arg	Gly	Trp	35	40	45	
Val	Trp	Asn	Gln	Phe	Phe	Val	Pro	Glu	Glu	Met	Asn	Thr	Thr	Ser	50	55	60	
His	His	Ile	Gly	Gln	Leu	Arg	Ser	Asp	Leu	Asp	Asn	Gly	Asn	Asn	65	70	75	
Ser	Phe	Gln	Tyr	Lys	Leu	Leu	Gly	Ala	Gly	Ala	Gly	Ser	Thr	Phe	80	85	90	
Ile	Ile	Asp	Glu	Arg	Thr	Gly	Asp	Ile	Tyr	Ala	Ile	Gln	Lys	Leu	95	100	105	
Asp	Arg	Glu	Glu	Arg	Ser	Leu	Tyr	Ile	Leu	Arg	Ala	Gln	Val	Ile	110	115	120	
Asp	Ile	Ala	Thr	Gly	Arg	Ala	Val	Glu	Pro	Glu	Ser	Glu	Phe	Val	125	130	135	
Ile	Lys	Val	Ser	Asp	Ile	Asn	Asp	Asn	Glu	Pro	Lys	Phe	Leu	Asp	140	145	150	
Glu	Pro	Tyr	Glu	Ala	Ile	Val	Pro	Glu	Met	Ser	Pro	Glu	Gly	Thr	155	160	165	
Leu	Val	Ile	Gln	Val	Thr	Ala	Ser	Asp	Ala	Asp	Asp	Pro	Ser	Ser	170	175	180	
Gly	Asn	Asn	Ala	Arg	Leu	Leu	Tyr	Ser	Leu	Leu	Gln	Gly	Gln	Pro	185	190	195	
Tyr	Phe	Ser	Val	Glu	Pro	Thr	Thr	Gly	Val	Ile	Arg	Ile	Ser	Ser	200	205	210	
Lys	Met	Asp	Arg	Glu	Leu	Gln	Asp	Glu	Tyr	Trp	Val	Ile	Ile	Gln	215	220	225	
Ala	Lys	Asp	Met	Ile	Gly	Gln	Pro	Gly	Ala	Leu	Ser	Gly	Thr	Thr	230	235	240	
Ser	Val	Leu	Ile	Lys	Leu	Ser	Asp	Val	Asn	Asp	Asn	Lys	Pro	Ile	245	250	255	
Phe	Lys	Glu	Ser	Leu	Tyr	Arg	Leu	Thr	Val	Ser	Glu	Ser	Ala	Pro	260	265	270	
Thr	Gly	Thr	Ser	Ile	Gly	Thr	Ile	Met	Ala	Tyr	Asp	Asn	Asp	Ile	275	280	285	

Gly	Glu	Asn	Ala	Glu	Met	Asp	Tyr	Ser	Ile	Glu	Glu	Asp	Asp	Ser	
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Gln	Thr	Phe	Asp	Ile	Ile	Thr	Asn	His	Glu	Thr	Gln	Glu	Gly	Ile	
				305					310					315	
Val	Ile	Leu	Lys	Lys	Lys	Val	Asp	Phe	Glu	His	Gln	Asn	His	Tyr	
				320					325					330	
Gly	Ile	Arg	Ala	Lys	Val	Lys	Asn	His	His	Val	Pro	Glu	Gln	Leu	
				335					340					345	
Met	Lys	Tyr	His	Thr	Glu	Ala	Ser	Thr	Thr	Phe	Ile	Lys	Ile	Gln	
				350					355					360	
Val	Glu	Asp	Val	Asp	Glu	Pro	Pro	Leu	Phe	Leu	Leu	Pro	Tyr	Tyr	
				365					370					375	
Val	Phe	Glu	Val	Phe	Glu	Glu	Thr	Pro	Gln	Gly	Ser	Phe	Val	Gly	
				380					385					390	
Val	Val	Ser	Ala	Thr	Asp	Pro	Asp	Asn	Arg	Lys	Ser	Pro	Ile	Arg	
				395					400					405	
Tyr	Ser	Ile	Thr	Arg	Ser	Lys	Val	Phe	Asn	Ile	Asn	Asp	Asn	Gly	
				410					415					420	
Thr	Ile	Thr	Thr	Ser	Asn	Ser	Leu	Asp	Arg	Glu	Ile	Ser	Ala	Trp	
				425					430					435	
Tyr	Asn	Leu	Ser	Ile	Thr	Ala	Thr	Glu	Lys	Tyr	Asn	Ile	Glu	Gln	
				440					445					450	
Ile	Ser	Ser	Ile	Pro	Leu	Tyr	Val	Gln	Val	Leu	Asn	Ile	Asn	Asp	
				455					460					465	
His	Ala	Pro	Glu	Phe	Ser	Gln	Tyr	Tyr	Glu	Thr	Tyr	Val	Cys	Glu	
				470					475					480	
Asn	Ala	Gly	Ser	Gly	Gln	Val	Ile	Gln	Thr	Ile	Ser	Ala	Val	Asp	
				485					490					495	
Arg	Asp	Glu	Ser	Ile	Glu	Glu	His	His	Phe	Tyr	Phe	Asn	Leu	Ser	
				500					505					510	
Val	Glu	Asp	Thr	Asn	Asn	Ser	Ser	Phe	Thr	Ile	Ile	Asp	Asn	Gln	
				515					520					525	
Asp	Asn	Thr	Ala	Val	Ile	Leu	Thr	Asn	Arg	Thr	Gly	Phe	Asn	Leu	
				530					535					540	
Gln	Glu	Glu	Pro	Val	Phe	Tyr	Ile	Ser	Ile	Leu	Ile	Ala	Asp	Asn	
				545					550					555	
Gly	Ile	Pro	Ser	Leu	Thr	Ser	Thr	Asn	Thr	Leu	Thr	Ile	His	Val	
				560					565					570	

Cys	Asp	Cys	Gly	Asp	Ser	Gly	Ser	Thr	Gln	Thr	Cys	Gln	Tyr	Gln	
				575					580					585	
Glu	Leu	Val	Leu	Ser	Met	Gly	Phe	Lys	Thr	Glu	Val	Ile	Ile	Ala	
				590					595					600	
Ile	Leu	Ile	Cys	Ile	Met	Ile	Ile	Phe	Gly	Phe	Ile	Phe	Leu	Thr	
				605					610					615	
Leu	Gly	Leu	Lys	Gln	Arg	Arg	Lys	Gln	Ile	Leu	Phe	Pro	Glu	Lys	
				620					625					630	
Ser	Glu	Asp	Phe	Arg	Glu	Asn	Ile	Phe	Gln	Tyr	Asp	Asp	Glu	Gly	
				635					640					645	
Gly	Gly	Glu	Glu	Asp	Thr	Glu	Ala	Phe	Asp	Ile	Ala	Glu	Leu	Arg	
				650					655					660	
Ser	Ser	Thr	Ile	Met	Arg	Glu	Arg	Lys	Thr	Arg	Lys	Thr	Thr	Ser	
				665					670					675	
Ala	Glu	Ile	Arg	Ser	Leu	Tyr	Arg	Gln	Ser	Leu	Gln	Val	Gly	Pro	
				680					685					690	
Asp	Ser	Ala	Ile	Phe	Arg	Lys	Phe	Ile	Leu	Glu	Lys	Leu	Glu	Glu	
				695					700					705	
Ala	Asn	Thr	Asp	Pro	Cys	Ala	Pro	Pro	Phe	Asp	Ser	Leu	Gln	Thr	
				710					715					720	
Tyr	Ala	Phe	Glu	Gly	Thr	Gly	Ser	Leu	Ala	Gly	Ser	Leu	Ser	Ser	
				725					730					735	
Leu	Glu	Ser	Ala	Val	Ser	Asp	Gln	Asp	Glu	Ser	Tyr	Asp	Tyr	Leu	
				740					745					750	
Asn	Glu	Leu	Gly	Pro	Arg	Phe	Lys	Arg	Leu	Ala	Cys	Met	Phe	Gly	
				755					760					765	
Ser	Ala	Val	Gln	Ser	Asn	Asn									
				770											

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 <211> 349  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 24, 60, 141, 226, 228, 249, 252  
 <223> unknown base

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attcaagcca aggacatgat tggtcagcca ggagcgttgt ntggaacaac 150  
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<210> 266

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 266

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<210> 267

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 267

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<211> 52

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<223> Synthetic oligonucleotide probe

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<210> 269

<211> 2747

<212> DNA

<213> Homo sapiens

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cccgccttaa cttcctccgc ggggccccagc caccttcggg agtccgggtt 150



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<212> PRT  
<213> Homo sapiens

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Arg Ile Tyr Ser Tyr Ala Gly Asp Asn Ile Val Thr Ala Gln Ala	35	40	45
Met Tyr Glu Gly Leu Trp Met Ser Cys Val Ser Gln Ser Thr Gly	50	55	60
Gln Ile Gln Cys Lys Val Phe Asp Ser Leu Leu Asn Leu Ser Ser	65	70	75
Thr Leu Gln Ala Thr Arg Ala Leu Met Val Val Gly Ile Leu Leu	80	85	90
Gly Val Ile Ala Ile Phe Val Ala Thr Val Gly Met Lys Cys Met	95	100	105
Lys Cys Leu Glu Asp Asp Glu Val Gln Lys Met Arg Met Ala Val	110	115	120
Ile Gly Gly Ala Ile Phe Leu Leu Ala Gly Leu Ala Ile Leu Val	125	130	135
Ala Thr Ala Trp Tyr Gly Asn Arg Ile Val Gln Glu Phe Tyr Asp	140	145	150
Pro Met Thr Pro Val Asn Ala Arg Tyr Glu Phe Gly Gln Ala Leu	155	160	165
Phe Thr Gly Trp Ala Ala Ala Ser Leu Cys Leu Leu Gly Gly Ala	170	175	180
Leu Leu Cys Cys Ser Cys Pro Arg Lys Thr Thr Ser Tyr Pro Thr	185	190	195
Pro Arg Pro Tyr Pro Lys Pro Ala Pro Ser Ser Gly Lys Asp Tyr	200	205	210

Val

<210> 271  
 <211> 564  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 21, 69, 163, 434, 436, 444  
 <223> unknown base

<400> 271  
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 ggatggatcg gcgccatcnt cacactgccc ttccccagtg gaggatttta 100  
 ctccctatgc tggcgacaac atcgtgaccg cccagcccat gtacgagggg 150

ctgtggatgt ccngcgtgtc gcagagcacc gggcagatcc agtgcaaagt 200  
ctttgactcc ttgctgaatc tgagcagcac attgcaagca acccgtgcct 250  
tgatgggtggg tggcatcctc ctgggagtga tagcaatctt tgtggccacc 300  
gttggcatga agtgtatgaa gtgcttgga gacgatgagg tgcagaagat 350  
gaggatggct gtcattgggg gcgcgatatt tcttcttgca ggtctggcta 400  
ttttagttgc cacagcatgg tatggcaata gaancnttca acanttctat 450  
gaccctatga cccagtcaa tgccaggtag gaatttggtc aggctctctt 500  
cactggctgg gctgctgctt ctctctgcct tctgggaggt gccctacttt 550  
gctgttctctg tccc 564

<210> 272  
<211> 498  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 30, 49, 102, 141, 147, 171, 324-325, 339-341  
<223> unknown base

<400> 272  
acccttgacc caacgcggcc ccccgaccgn ttcattggcca aacgcgggnc 50  
tccagctgtt gggcttcatt ctccccctcc tgggatggac cggcgcccat 100  
cntcagcact gccctgcccc agtggaggat ttactcctat nccggcnaca 150  
acatcgtgac cgcccaggcc ntgtacgagg ggctgtggat gtccctgcgtg 200  
tcgcagagca ccgggcagat ccagtgcaaa gtctttgact cccttgctga 250  
atctgagcag cacattgcaa gcaaccctg ccttgatggg ggttggcatc 300  
ctcctgggag tgatagcaat cttnttgcc accgttgtnn ntgaagtgt 350  
tgaagtgcct ggaagacgat gaggtgcaga agatgaggat ggctgtcatt 400  
gggggcgcga tatttcttct tgcaggtctg gctatcttag ttgccacagc 450  
atggtatggc aatagaatcg ttcaagaatt ctatgaccct atgaccga 498

<210> 273  
<211> 552  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure

<222> 25, 57, 67, 94-95, 116, 152, 165, 212, 233, 392-394

<223> unknown base

<400> 273

gggcccgacc attatccaac cgggntcact gttgggtcat ctccctcctg 50  
gatgaancgc gccatcntca gactccctgc cccatggaga tttnnccat 100  
gctggcgaca acatcntgac ccccagccat gtacgagggg ctttgaacgt 150  
cngcgtgtcg cagancaccg ggcagatcca gtgcaaagtc tttgactcct 200  
tgctgaatct gngcagcaca ttgcagcaac cntgcccctg atgggtggtg 250  
gcatcctcct gggagtgata gcaatctttg tggccaccgt tggcatgaag 300  
tgtatgaagt gcttgggaaga cgatgaggtg cagaagatga ggatggctgt 350  
cattgggggc gcgatatttc ttcttgacag tctggctatt tnnngttgcc 400  
acagcatggt atggcaatag aatcgttcaa gaattctatg accctatgac 450  
cccagtcaat gccaggtagc aatttggtca ggctctcttc actggctggg 500  
ctgctgcttc tctctgcctt ctgggaggtg ccctactttg ctgttcctgc 550  
ga 552

<210> 274

<211> 526

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 25, 50, 60, 123, 127, 370, 395, 397-398, 402-403, 405-407

<223> unknown base

<400> 274

atttccccct cctggatgga tgcgccacc gtcacattgc cttccccan 50  
tggaggattn actcctatgc tggcgacaac atcgtgacct cccaggccat 100  
ttaccgaggg gctttggatg tcntgcntgt cgcagagcac cgggcagatc 150  
ccagtgcaaa gtctttgact ccttgctgaa tctgagcagc acattgcaag 200  
caaccctgac cttgatgggg ttggcatcct cctgggagtg atagcaacct 250  
ttgtggccac cggtggcatg aagtgtatga agtgcttga agacgatgag 300  
gtgccagaag atgaggatgg ctgtcattgg gggcgcgata tttcttggtg 350  
caggtctggc tatttttagtn gccacagcat ggtatggcaa tagantnntt 400  
cnnngnntct atgaccctat gacccagtc aatgccaggt acgaatttgg 450

tcaggctctc ttcactgggt gggctgctgc ttctctctgc cttctgggag 500  
gtgccctact ttgctgttcc tgtccc 526

<210> 275  
<211> 398  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 22, 61, 91, 144, 238-239, 262, 265-266, 271, 274  
<223> unknown base

<400> 275  
agagcaccgg cagatcccag tncaaagtct ttgacccttg ctgaatctga 50  
gcagcacatt ncaagcaacc ccttgcccttg aaggtgggtg ncatcccccc 100  
tgggagtgaa tagcaatctt tgtggccacc gttggcatga agtntatgaa 150  
gtgcttggaa gacgatgagg tgcagaagat gaggatggct gtcattgggg 200  
gcgcgatatt tcttcttgca ggtctggcta ttttagtnnc cacagcatgg 250  
tatggcaata gnatnnttcg nggnttctat gaccctatga cccagtcaa 300  
tgccaggtag gaatttgggc aggtctctct cactggctgg gctgctgctt 350  
ctctctgcct tctgggaggt gccctacttt gctgttcttg tccccgaa 398

<210> 276  
<211> 495  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 39, 58, 130, 234, 314, 364, 427, 450, 461, 476  
<223> unknown base

<400> 276  
agcaatgccc tgccccaggt ggaggattaa ttcctatgnt ggggacaaca 50  
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cagagcaccg ggcagatcca gtgcaaagtn tttgactcct tgctgaattt 150  
gagcagcaca ttgcaagcaa cccgtgcctt gatggtgggt ggcattcttc 200  
tgggagtgat agcaatcttt gtggccaccg tggnaatgaa gtgtatgaag 250  
tgcttgggaag acgatgaggt gcagaagatg aggatggctg tcattggggg 300  
cgcgatattt cttnttgcag gtctggctat tttagttgcc acagcatggt 350  
atggcaatag aatngttcaa gaattttatg accctatgac cccagtcaat 400

gccaggtacg aatttgggtca ggctttnttc actggctggg ctgctgcttn 450

tttctgcctt ntgggaggtg ccctantttg ctgttcctgc gaacc 495

<210> 277

<211> 200

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 34, 87, 138, 147, 163, 165-166, 172

<223> unknown base

<400> 277

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cacagcatgg tatggcaata gaatcggtca agaattntat gaccctatga 100

ccccagtcaa tgccaggtac gaatttgggc aggcctctntt cactggntgg 150

gctgctgctt ctntnngcct tntgggaggt gccctacttt gctgttcctg 200

<210> 278

<211> 542

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 26, 43, 55, 77, 198, 361-362, 391-392, 396

<223> unknown base

<400> 278

ttcctgggat ggatccgccc ccactntcac atgccctgcc cnttggagat 50

ttacncctat gctggcgaaac aacatcntga ccgcccaggc catgtacgag 100

gggctgtgga atgtcctgcg tgtcccagag caccgggcag atccagtgc 150

aagtctttga ctcttgctg aatctgagca gcacattgca agcaacntg 200

ccttgatggg ggttggcatc ctctgggag tgatagcaat ctttgtggcc 250

accgttggca tgaaagtgt tgaagtgctt ggaagacgat gaggtgcaga 300

agatgaggat ggctgtcatt gggggcgaga tatttcttct tgcaggctctg 350

gctattttag nngccacagc atgggtatggc aatcagaccc nntcanaaac 400

tctatgaccc tatgacccca gtcaatgcc ggtacgaatt tggtcaggct 450

ctcttcactg gctgggctgc tgcttctctc tgcttcttgg gaggtgccct 500

actttgctgt tcctgtcccc gaaaaacaac ctcttaccga cg 542

<210> 279  
<211> 548  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 90, 115, 147, 228, 387  
<223> unknown base

<400> 279  
cggggctgca gctggtgggc ttcattctgc ttcctgggat ggaatcggcg 50  
ccatcgtcag cactgccctg ccccatggag gatttactcn tatgctggcg 100  
acaacatcgt gaccnccag gccatgtacg aggggctgtg gatgtcngcg 150  
tgtcgcagag caccgggcag atccagtgc aagtctttga ctcttgctg 200  
aatctgagca gcacattgca agcaacctg ccttgatggt ggttggcatc 250  
ctctggggag tgatagcaat ctttgtggcc accgttggca tgaagtgtat 300  
gaagtgcttg gaagacgatg aggtgcagaa gatgaggatg gctgtcattg 350  
ggggcgcgat atttcttctt gcaggctctg ctatttntag ttgccacagc 400  
atgggatggc aatagaatcg ttcaagaatt ctatgaccct atgaccccag 450  
tcaatgccag gtacgaattt ggtcaggctc tcttcactgg ctgggctgct 500  
gctttctctct gccttctggg aggtgcccta ctttgcgtgt cctgcgaa 548

<210> 280  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 280  
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<210> 281  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 281  
gtgtcacacg tagtctttcc cgctgg 26

<210> 282  
<211> 43



<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 282  
ctgcagctgt tgggcttcat tctcgccttc ctgggatgga tcg 43

<210> 283  
<211> 2285  
<212> DNA  
<213> Homo sapiens

<400> 283  
gcgtgccgtc agctcgccgg gcaccggggc ctgccctcg ccctccgccc 50  
ctgcgcctgc accgcgtaga ccgaccccc cctccagcgc gccacccgg 100  
tagaggaccc ccgcccgtgc ccgacccggt cccgccttt ttgtaaaact 150  
taaagcgggc gcagcattaa cgcttccgc cccggtgacc tctcaggggt 200  
ctccccgcca aaggtgctcc gccgctaagg aacatggcga aggtggagca 250  
ggctctgagc ctcgagccgc agcacgagct caaattccga ggtcccttca 300  
ccgatgttgt caccaccaac ctaaagcttg gcaaccgac agaccgaaat 350  
gtgtgtttta aggtgaagac tacagcacca cgtaggtact gtgtgaggcc 400  
caacagcggg atcatcgatg caggggcctc aattaatgta tctgtgatgt 450  
tacagccttt cgattatgat cccaatgaga aaagtaaaca caagtttatg 500  
gttcagtcta tgtttgctcc aactgacact tcagatatgg aagcagtatg 550  
gaaggaggca aaaccggaag accttatgga ttcaaaactt agatgtgtgt 600  
ttgaattgcc agcagagaat gataaaccac atgatgtaga aataaataaa 650  
attatatcca caactgcac aaagacagaa acaccaatag tgtctaagtc 700  
tctgagttct tctttggatg acaccgaagt taagaagggt atggaagaat 750  
gtaagaggct gcaaggtgaa gttcagaggc tacgggagga gaacaagcag 800  
ttcaaggaag aagatggact gcggatgagg aagacagtgc agagcaacag 850  
ccccatttca gcattagccc caactgggaa ggaagaaggc cttagcacc 900  
ggctcttggc tctggtggtt ttgttcttta tcgttggtgt aattattggg 950  
aagattgcct tgtagaggta gcatgcacag gatggtaaata tggattggtg 1000  
gatccaccat atcatgggat ttaaatttat cataaccatg tgtaaaaaga 1050

aattaatgta tgatgacatc tcacaggtct tgcctttaaa ttacccctcc 1100  
ctgcacacac atacacagat acacacacac aaatataatg taacgatctt 1150  
ttagaaagt aaataatgtat agtaactgat tgagggggaa aaagaatgat 1200  
ctttattaat gacaaggga accatgagta atgccacaat ggcatattgt 1250  
aaatgtcatt ttaaacattg gtaggccttg gtacatgatg ctggattacc 1300  
tctcttaaaa tgacaccctt cctcgcctgt tgggtgctggc ccttggggag 1350  
ctggagccca gcatgctggg gagtgcggtc agctccacac agtagtccc 1400  
acgtggccca ctcccgccc aggtgcttt ccgtgtcttc agttctgtcc 1450  
aagccatcag ctcttggga ctgatgaaca gagtcagaag cccaaaggaa 1500  
ttgcactgtg gcagcatcag acgtactcgt cataagtga aggcgtgtgt 1550  
tgactgattg acccagcgt ttggaaataa atggcagtgc tttgttcact 1600  
taaagggacc aagctaaatt tgtattggtt catgtagtga agtcaaactg 1650  
ttattcagag atgtttaatg catatttaac ttatttaatg tatttcact 1700  
catgttttct tattgtcaca agagtacagt taatgctgcg tgctgctgaa 1750  
ctctgttggg tgaactggta ttgctgctgg agggctgtgg gctcctctgt 1800  
ctctggagag tctggtcatg tggaggtggg gtttattggg atgctggaga 1850  
agagctgcca ggaagtgttt tttctgggtc agtaaataac aactgtcata 1900  
gggagggaaa ttctcagtag tgacagtcaa ctctaggtta ctttttttaa 1950  
tgaagagtag tcagtcttct agattgttct tataccacct ctcaaccatt 2000  
actcacactt ccagcgccca ggtccaagtc tgagcctgac ctccccttgg 2050  
ggacctagcc tggagtcagg acaaatggat cgggctgcag agggttagaa 2100  
gcgagggcac cagcagttgt ggggtggggag caagggaaga gagaaactct 2150  
tcagcgaatc cttctagtag tagttgagag tttgactgtg aattaatttt 2200  
atgccataaa agaccaacc agttctgttt gactatgtag catcttgaaa 2250  
agaaaaatta taataaagcc ccaaaattaa gaaaa 2285

<210> 284

<211> 243

<212> PRT

<213> Homo sapiens

<400> 284

Met Ala Lys Val Glu Gln Val Leu Ser Leu Glu Pro Gln His Glu

1	5	10	15
Leu Lys Phe Arg Gly	Pro Phe Thr Asp	Val Val Thr Thr Asn	Leu
20		25	30
Lys Leu Gly Asn Pro	Thr Asp Arg Asn	Val Cys Phe Lys Val	Lys
35		40	45
Thr Thr Ala Pro Arg	Arg Tyr Cys Val	Arg Pro Asn Ser Gly	Ile
50		55	60
Ile Asp Ala Gly Ala	Ser Ile Asn Val	Ser Val Met Leu Gln	Pro
65		70	75
Phe Asp Tyr Asp Pro	Asn Glu Lys Ser	Lys His Lys Phe Met	Val
80		85	90
Gln Ser Met Phe Ala	Pro Thr Asp Thr	Ser Asp Met Glu Ala	Val
95		100	105
Trp Lys Glu Ala Lys	Pro Glu Asp Leu	Met Asp Ser Lys Leu	Arg
110		115	120
Cys Val Phe Glu Leu	Pro Ala Glu Asn	Asp Lys Pro His Asp	Val
125		130	135
Glu Ile Asn Lys Ile	Ile Ser Thr Thr	Ala Ser Lys Thr Glu	Thr
140		145	150
Pro Ile Val Ser Lys	Ser Leu Ser Ser	Ser Leu Asp Asp Thr	Glu
155		160	165
Val Lys Lys Val Met	Glu Glu Cys Lys	Arg Leu Gln Gly Glu	Val
170		175	180
Gln Arg Leu Arg Glu	Glu Asn Lys Gln	Phe Lys Glu Glu Asp	Gly
185		190	195
Leu Arg Met Arg Lys	Thr Val Gln Ser	Asn Ser Pro Ile Ser	Ala
200		205	210
Leu Ala Pro Thr Gly	Lys Glu Glu Gly	Leu Ser Thr Arg Leu	Leu
215		220	225
Ala Leu Val Val Leu	Phe Phe Ile Val	Gly Val Ile Ile Gly	Lys
230		235	240

Ile Ala Leu

<210> 285

<211> 418

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 40, 53, 68, 119, 134, 177-178, 255

<223> unknown base

<400> 285

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tcnagcgccc aggtccangt ctgagcctga cttccccttg gggacctagc 100  
ctggagtcag gacaatggnt cgggctgcag aggnntagaa gcgagggcac 150  
cagcagtttt ggggtggggag caagggnnga gagaaactct tcagcgaatc 200  
cttctagtag tagttgagag tttgactgtg aattaatttt atgccataaa 250  
agacnaaccc agttctgttt gactatgtag catcttgaaa agaaaaatta 300  
taataaagcc ccaaaattaa gaattctttt gtcattttgt cacatttgct 350  
ctatgggggg aattattatt ttatcatttt tattattttg ccattggaag 400  
gttaacttta aaatgagc 418

<210> 286

<211> 543

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 73, 97

<223> unknown base

<400> 286

tattgtaaag gccattttaa accattggta ggccttgga catgatgctg 50  
gattacctcc ttaaagaca cnttcctcg cctggtggtg ctggcconttg 100  
gggagctgga gccccagcat gctggggagt gcggtcagct ccacacagta 150  
gtccccacgt ggcccactcc cggcccaggc tgctttccgt gtcttcagtt 200  
ctgtccaagc catcagctcc ttgggactga tgaacagagt cagaagccca 250  
aaggaattgc cactgtggca gcatcagacg tactcgtcat aagtgagagg 300  
cgtgtgttga ctgattgacc cagcgctttg gaaataaatg gcagtgcctt 350  
gttcacttaa agggaccaag ctaaattgta ttggttcatg tagtgaagtc 400  
aaactgttat tcagagatgt ttaatgcata tttaacttat ttaatgtatt 450  
tcatctcatg ttttcttatt gtcacaagag tacagttaat gctgcgtgct 500  
gctgaactct gttgggtgaa ctggtattgc tgctggaggg ctg 543

<210> 287

<211> 270

<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 38, 64, 72, 164, 198, 200, 220, 222, 229, 242  
<223> unknown base

<400> 287  
ccctggtggt tttgttcttt aattcgttgg tgtaattntt gggaagattg 50  
cttgtagagg tagnatgcac cnggctggta aattggattg gtggatccac 100  
catatccatg ggattttaaatttatacataac catgtgtaaa aagaaattaa 150  
tgtatgatga catntcacag gtattgcctt taaattaccc atccctgnan 200  
acacatacac agatacacan anacaaatnt aatgtaacga tnttttagaa 250  
agttaaaaat gtatagtaac 270

<210> 288  
<211> 428  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 35, 116, 129, 197, 278, 294, 297, 349, 351  
<223> unknown base

<400> 288  
ggtggcccat tcccggccca ggctgctttc cggtnttcag ttctgtccaa 50  
gccatcagct ccttgggact gatgaacaga gtcagaagcc caaaggaatt 100  
gcaactgtggc agcatnagac gtacttgtna taagtgagag gcgtgtgttg 150  
actgattgac ccagcgcttt ggaaataaat ggcagtgcctt tgttcantta 200  
aagggaccaa gctaaatttg tattggttca tgtagtgaag tcaaactgtt 250  
attcagagat gtttaatgca tttttaantt atttaatgta tttnatntca 300  
tgttttctta ttgtcacaag agtacagtta atgctgcgtg ctgctgaant 350  
ntgttgggtg aactgggtatt gctgctggag ggctgtgggc tcctctgtct 400  
ttggagagtc tggatcatgtg gaggtggg 428

<210> 289  
<211> 320  
<212> DNA  
<213> Homo sapiens

<400> 289  
tgctttccgt gtcttcagtt ctgtccaagc catcagctcc ttgggacttg 50

atgaacagag tcagaagccc aaaggaattg cactgtggca gcatcagacg 100  
tactcgtcat aagtgaagagg cgtgtgttga ctgattgacc cagcgctttg 150  
gaaataaatg gcagtgcctt gttcacttaa agggaccaag ctaaatttgt 200  
attggttcat gtagtgaagt caaactgtta ttcagagatg tttaatgcat 250  
atttaactta tttaatgtat ttcattctcat gttttcttat tgtcacaaga 300  
gtacagttaa tgctgcgtgc 320

<210> 290

<211> 609

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 57, 60, 186, 235, 244, 304, 339, 355, 359, 361, 387, 432, 441,  
447, 481, 513, 532, 584, 598

<223> unknown base

<400> 290

aaacctttaa aagttgaggg gaaaagaatg atcctttatt aatgacaagg 50  
gaaaccntgn gtaatgccac aatggcatat tgtaaattgc attttaaaaca 100  
ttggtagggc ttggtacatg atgctggatt acctctctta aaatgacacc 150  
cttctctgcc tgttggtgct ggcccttggg gagctngagc ccagcatgct 200  
ggggagtgcg gtctgctcca cacagtagtc cccangtggc ccantcccgg 250  
cccaggctgc tttccgtgct ttcagttctg tccaagccat cagctccttg 300  
ggantgatga acagagtcag aagcccaaag gaattgcant gtggcagcat 350  
cagangtant ngtcataagt gagaggcgtg tgttgantga ttgaccacgc 400  
gctttggaaa taaatggcag tgctttgttc anttaaaggg nccaagntaa 450  
atgtgtattg gttcatgtag tgaagtcaaa ntgttattca gagatgttta 500  
atgcatattt aanttattta atgtatttca tntcatgttt tcttattgtc 550  
acaagggtac agttaatgct gcgtgctgct gaantctgtt gggagaantg 600  
gtattgctg 609

<210> 291

<211> 493

<212> DNA

<213> Homo sapiens

<400> 291

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cacagtagtc cccacgtggc ccaactcccgg ccagagctgc tttccgtgtc 100  
ttcagttctg tccaagccat cagctccttg ggactgatga acagagtcag 150  
aagcccaaag gaattgcact gtggcagcat cagacgtact cgtcataagt 200  
gagaggcgtg tgttgactga ttgaccacgc gctttggaaa taaatggcag 250  
tgctttgttc acttaaaggg accaagctaa atttgtattg gttcatgtag 300  
tgaagtcaaa ctgttattca gagatgttta atgcatattt aacttattta 350  
atgtatttca tctcatgttt tcttattgtc acaagagtac agttaatgct 400  
gcgtgctgct gaactctggt ggggtgaactg gtattgctgc tggagggctg 450  
tgggctcctc tgtctctgga gagtctggtc atgtggaggt ggg 493

<210> 292

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 292

gcaccaccgt aggtacttgt gtgaggc 27

<210> 293

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 293

aaccaccaga gccaagagcc ggg 23

<210> 294

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 294

cagcggaatc atcgatgcag gggcctcaat taatgtatct gtgatgttac 50

<210> 295

<211> 2530

<212> DNA

<213> Homo sapiens

<400> 295

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gtctcacttt gttgccaggt ctggagttca gtgccatgat catggtttac 200  
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atttttcacc cctgggtgga cctcattga tggatctgaa atggaatggg 350  
attttatgtg gcacttgaga aaggtacccc ggattgtcag tgaaaggact 400  
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 aatgtgaaat tgcatagata aaggtagatg gtaaagcaat tagtatcaga 1950  
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<210> 296  
 <211> 413  
 <212> PRT  
 <213> Homo sapiens

<400> 296  
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Thr Ser Pro Ala Phe Glu Ala Asp Ala Lys Met Met Val Asn Thr	50	55	60
Val Cys Gly Ile Glu Cys Gln Lys Glu Leu Pro Thr Pro Ser Leu	65	70	75
Ser Glu Leu Glu Asp Tyr Leu Ser Tyr Glu Thr Val Phe Glu Asn	80	85	90
Gly Thr Arg Thr Leu Thr Arg Val Lys Val Gln Asp Leu Val Leu	95	100	105
Glu Pro Thr Gln Asn Ile Thr Thr Lys Gly Val Ser Val Arg Arg	110	115	120
Lys Arg Gln Val Tyr Gly Thr Asp Ser Arg Phe Ser Ile Leu Asp	125	130	135
Lys Arg Phe Leu Thr Asn Phe Pro Phe Ser Thr Ala Val Lys Leu	140	145	150
Ser Thr Gly Cys Ser Gly Ile Leu Ile Ser Pro Gln His Val Leu	155	160	165
Thr Ala Ala His Cys Val His Asp Gly Lys Asp Tyr Val Lys Gly	170	175	180
Ser Lys Lys Leu Arg Val Gly Leu Leu Lys Met Arg Asn Lys Ser	185	190	195
Gly Gly Lys Lys Arg Arg Gly Ser Lys Arg Ser Arg Arg Glu Ala	200	205	210
Ser Gly Gly Asp Gln Arg Glu Gly Thr Arg Glu His Leu Gln Glu	215	220	225
Arg Ala Lys Gly Gly Arg Arg Arg Lys Lys Ser Gly Arg Gly Gln	230	235	240
Arg Ile Ala Glu Gly Arg Pro Ser Phe Gln Trp Thr Arg Val Lys	245	250	255
Asn Thr His Ile Pro Lys Gly Trp Ala Arg Gly Gly Met Gly Asp	260	265	270
Ala Thr Leu Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Arg Ala	275	280	285
His Lys Lys Lys Tyr Met Glu Leu Gly Ile Ser Pro Thr Ile Lys	290	295	300
Lys Met Pro Gly Gly Met Ile His Phe Ser Gly Phe Asp Asn Asp			

305	310	315
Arg Ala Asp Gln Leu Val Tyr Arg Phe	Cys Ser Val Ser Asp Glu	
320	325	330
Ser Asn Asp Leu Leu Tyr Gln Tyr Cys	Asp Ala Glu Ser Gly Ser	
335	340	345
Thr Gly Ser Gly Val Tyr Leu Arg Leu	Lys Asp Pro Asp Lys Lys	
350	355	360
Asn Trp Lys Arg Lys Ile Ile Ala Val	Tyr Ser Gly His Gln Trp	
365	370	375
Val Asp Val His Gly Val Gln Lys Asp	Tyr Asn Val Ala Val Arg	
380	385	390
Ile Thr Pro Leu Lys Tyr Ala Gln Ile	Cys Leu Trp Ile His Gly	
395	400	405
Asn Asp Ala Asn Cys Ala Tyr Gly		
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<210> 297

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 297

gcatctgcag gagagagcga aggg 24

<210> 298

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 298

catcggtccc gtgaatccag aggc 24

<210> 299

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 299

gaagggaggc cttcctttca gtggacccgg gtcaagaata cccac 45

<210> 300

<211> 1869  
<212> DNA  
<213> Homo sapiens

<400> 300

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gcaactcctg gcacactgct cctctttctg gctttcctgc tcctgagttc 200
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 gtttaaagaa agcagtgtct cactgggtgt agctttcatg ggttctgaac 1800  
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 ttagtttcaa aaaaaaaaaa 1869

<210> 301  
 <211> 525  
 <212> PRT  
 <213> Homo sapiens

<400> 301  
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 Asp Arg Asp Gly Leu Trp Asp Ala Trp Gly Pro Trp Ser Glu Cys  
 35 40 45  
 Ser Arg Thr Cys Gly Gly Gly Ala Ser Tyr Ser Leu Arg Arg Cys  
 50 55 60  
 Leu Ser Ser Lys Ser Cys Glu Gly Arg Asn Ile Arg Tyr Arg Thr  
 65 70 75  
 Cys Ser Asn Val Asp Cys Pro Pro Glu Ala Gly Asp Phe Arg Ala  
 80 85 90  
 Gln Gln Cys Ser Ala His Asn Asp Val Lys His His Gly Gln Phe  
 95 100 105  
 Tyr Glu Trp Leu Pro Val Ser Asn Asp Pro Asp Asn Pro Cys Ser  
 110 115 120  
 Leu Lys Cys Gln Ala Lys Gly Thr Thr Leu Val Val Glu Leu Ala  
 125 130 135

Pro	Lys	Val	Leu	Asp	Gly	Thr	Arg	Cys	Tyr	Thr	Glu	Ser	Leu	Asp	
				140					145					150	
Met	Cys	Ile	Ser	Gly	Leu	Cys	Gln	Ile	Val	Gly	Cys	Asp	His	Gln	
				155					160					165	
Leu	Gly	Ser	Thr	Val	Lys	Glu	Asp	Asn	Cys	Gly	Val	Cys	Asn	Gly	
				170					175					180	
Asp	Gly	Ser	Thr	Cys	Arg	Leu	Val	Arg	Gly	Gln	Tyr	Lys	Ser	Gln	
				185					190					195	
Leu	Ser	Ala	Thr	Lys	Ser	Asp	Asp	Thr	Val	Val	Ala	Leu	Pro	Tyr	
				200					205					210	
Gly	Ser	Arg	His	Ile	Arg	Leu	Val	Leu	Lys	Gly	Pro	Asp	His	Leu	
				215					220					225	
Tyr	Leu	Glu	Thr	Lys	Thr	Leu	Gln	Gly	Thr	Lys	Gly	Glu	Asn	Ser	
				230					235					240	
Leu	Ser	Ser	Thr	Gly	Thr	Phe	Leu	Val	Asp	Asn	Ser	Ser	Val	Asp	
				245					250					255	
Phe	Gln	Lys	Phe	Pro	Asp	Lys	Glu	Ile	Leu	Arg	Met	Ala	Gly	Pro	
				260					265					270	
Leu	Thr	Ala	Asp	Phe	Ile	Val	Lys	Ile	Arg	Asn	Ser	Gly	Ser	Ala	
				275					280					285	
Asp	Ser	Thr	Val	Gln	Phe	Ile	Phe	Tyr	Gln	Pro	Ile	Ile	His	Arg	
				290					295					300	
Trp	Arg	Glu	Thr	Asp	Phe	Phe	Pro	Cys	Ser	Ala	Thr	Cys	Gly	Gly	
				305					310					315	
Gly	Tyr	Gln	Leu	Thr	Ser	Ala	Glu	Cys	Tyr	Asp	Leu	Arg	Ser	Asn	
				320					325					330	
Arg	Val	Val	Ala	Asp	Gln	Tyr	Cys	His	Tyr	Tyr	Pro	Glu	Asn	Ile	
				335					340					345	
Lys	Pro	Lys	Pro	Lys	Leu	Gln	Glu	Cys	Asn	Leu	Asp	Pro	Cys	Pro	
				350					355					360	
Ala	Ser	Asp	Gly	Tyr	Lys	Gln	Ile	Met	Pro	Tyr	Asp	Leu	Tyr	His	
				365					370					375	
Pro	Leu	Pro	Arg	Trp	Glu	Ala	Thr	Pro	Trp	Thr	Ala	Cys	Ser	Ser	
				380					385					390	
Ser	Cys	Gly	Gly	Gly	Ile	Gln	Ser	Arg	Ala	Val	Ser	Cys	Val	Glu	
				395					400					405	
Glu	Asp	Ile	Gln	Gly	His	Val	Thr	Ser	Val	Glu	Glu	Trp	Lys	Cys	
				410					415					420	

Met	Tyr	Thr	Pro	Lys	Met	Pro	Ile	Ala	Gln	Pro	Cys	Asn	Ile	Phe
				425					430					435
Asp	Cys	Pro	Lys	Trp	Leu	Ala	Gln	Glu	Trp	Ser	Pro	Cys	Thr	Val
				440					445					450
Thr	Cys	Gly	Gln	Gly	Leu	Arg	Tyr	Arg	Val	Val	Leu	Cys	Ile	Asp
				455					460					465
His	Arg	Gly	Met	His	Thr	Gly	Gly	Cys	Ser	Pro	Lys	Thr	Lys	Pro
				470					475					480
His	Ile	Lys	Glu	Glu	Cys	Ile	Val	Pro	Thr	Pro	Cys	Tyr	Lys	Pro
				485					490					495
Lys	Glu	Lys	Leu	Pro	Val	Glu	Ala	Lys	Leu	Pro	Trp	Phe	Lys	Gln
				500					505					510
Ala	Gln	Glu	Leu	Glu	Glu	Gly	Ala	Ala	Val	Ser	Glu	Glu	Pro	Ser
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<210> 302  
 <211> 1533  
 <212> DNA  
 <213> Homo sapiens

<400> 302  
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 ctggggcggg cgctgtggct ggcggcccgc cggttcgtgg ggcccaggg 150  
 ccagcggctg cgcagaggcg gggaccccg cctcatgcac gggaagactg 200  
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 aaaagctttt gttatagccg gagcaaactg gctaacattc tttttaccag 750

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<210> 303

<211> 336

<212> PRT

<213> Homo sapiens

<400> 303

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			20						25					30

Arg	Leu	Arg	Arg	Gly	Gly	Asp	Pro	Gly	Leu	Met	His	Gly	Lys	Thr
			35						40					45

Val	Leu	Ile	Thr	Gly	Ala	Asn	Ser	Gly	Leu	Gly	Arg	Ala	Thr	Ala
			50						55					60

Ala	Glu	Leu	Leu	Arg	Leu	Gly	Ala	Arg	Val	Ile	Met	Gly	Cys	Arg
			65						70					75

Asp	Arg	Ala	Arg	Ala	Glu	Glu	Ala	Ala	Gly	Gln	Leu	Arg	Arg	Glu
			80						85					90

Leu	Arg	Gln	Ala	Ala	Glu	Cys	Gly	Pro	Glu	Pro	Gly	Val	Ser	Gly
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Val	Gly	Glu	Leu	Ile	Val	Arg	Glu	Leu	Asp	Leu	Ala	Ser	Leu	Arg
				110					115					120
Ser	Val	Arg	Ala	Phe	Cys	Gln	Glu	Met	Leu	Gln	Glu	Glu	Pro	Arg
				125					130					135
Leu	Asp	Val	Leu	Ile	Asn	Asn	Ala	Gly	Ile	Phe	Gln	Cys	Pro	Tyr
				140					145					150
Met	Lys	Thr	Glu	Asp	Gly	Phe	Glu	Met	Gln	Phe	Gly	Val	Asn	His
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Leu	Gly	His	Phe	Leu	Leu	Thr	Asn	Leu	Leu	Leu	Gly	Leu	Leu	Lys
				170					175					180
Ser	Ser	Ala	Pro	Ser	Arg	Ile	Val	Val	Val	Ser	Ser	Lys	Leu	Tyr
				185					190					195
Lys	Tyr	Gly	Asp	Ile	Asn	Phe	Asp	Asp	Leu	Asn	Ser	Glu	Gln	Ser
				200					205					210
Tyr	Asn	Lys	Ser	Phe	Cys	Tyr	Ser	Arg	Ser	Lys	Leu	Ala	Asn	Ile
				215					220					225
Leu	Phe	Thr	Arg	Glu	Leu	Ala	Arg	Arg	Leu	Glu	Gly	Thr	Asn	Val
				230					235					240
Thr	Val	Asn	Val	Leu	His	Pro	Gly	Ile	Val	Arg	Thr	Asn	Leu	Gly
				245					250					255
Arg	His	Ile	His	Ile	Pro	Leu	Leu	Val	Lys	Pro	Leu	Phe	Asn	Leu
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Val	Ser	Trp	Ala	Phe	Phe	Lys	Thr	Pro	Val	Glu	Gly	Ala	Gln	Thr
				275					280					285
Ser	Ile	Tyr	Leu	Ala	Ser	Ser	Pro	Glu	Val	Glu	Gly	Val	Ser	Gly
				290					295					300
Arg	Tyr	Phe	Gly	Asp	Cys	Lys	Glu	Glu	Glu	Leu	Leu	Pro	Lys	Ala
				305					310					315
Met	Asp	Glu	Ser	Val	Ala	Arg	Lys	Leu	Trp	Asp	Ile	Ser	Glu	Val
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<210> 304  
 <211> 521  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure

<222> 20, 34, 62, 87, 221, 229

<223> unknown base

<400> 304

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gaattaagtg actcaaagtg ctatcgagag gtttttcaag tatctttgag 450  
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<210> 305

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 305

ccaggaaatg ctccaggaag agcc 24

<210> 306

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 306

gcccattgaca ccaaattgaa gagtgg 26

<210> 307

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 307

aacgcagggg tcttccagtg cccttacatg aagactgaag atggg 45

<210> 308

<211> 1523

<212> DNA

<213> Homo sapiens

<400> 308

gagaggacga ggtgccgctg cctggagaat cctccgctgc cgtcggctcc 50  
cggagcccag ccctttccta acccaaccca acctagccca gtcccagccg 100  
ccagcgctg tccctgtcac ggacccagc gttaccatgc atcctgccgt 150  
cttcctatcc ttaccgacc tcagatgctc ctttctgctc ctggtaactt 200  
gggtttttac tcctgtaaca actgaaataa caagtcttgc tacagagaat 250  
atagatgaaa ttttaaaca tgctgatgtt gctttagtaa atttttatgc 300  
tgactggtgt cgtttcagtc agatgttgca tccaatttt gaggaagctt 350  
ccgatgtcat taaggaagaa tttccaaatg aaaatcaagt agtgtttgcc 400  
agagttgatt gtgatcagca ctctgacata gccagagat acaggataag 450  
caaataccca accctcaa atgtttcgtaa tgggatgatg atgaagagag 500  
aatacagggg tcagcgatca gtgaaagcat tggcagatta catcaggcaa 550  
caaaaaagtg accccattca agaaattcgg gacttagcag aaatcaccac 600  
tcttgatcgc agcaaaaagaa atatcattgg atattttgag caaaaggact 650  
cggacaacta tagagttttt gaacgagtag cgaatatttt gcatgatgac 700  
tgtgcctttc tttctgcatt tggggatgtt tcaaaaccgg aaagatatag 750  
tggcgacaac ataatctaca aaccaccagg gcattctgct ccggatatgg 800  
tgtacttggg agctatgaca aattttgatg tgacttaca ttggattcaa 850  
gataaatgtg ttctcttgt ccgagaaata acatttgaaa atggagagga 900  
attgacagaa gaaggactgc cttttctcat actctttcac atgaaagaag 950  
atacagaaag tttagaaata ttccagaatg aagtagctcg gcaattaata 1000  
agtgaaaaag gtacaataaa ctttttacat gccgattgtg acaaatttag 1050  
acatcctctt ctgcacatac agaaaactcc agcagattgt cctgtaatcg 1100  
ctattgacag ctttaggc atgtatgtgt ttggagactt caaagatgta 1150  
ttaattcctg gaaaactcaa gcaattcgta tttgacttac attctggaaa 1200  
actgcacaga gaattccatc atggacctga cccaactgat acagccccag 1250

gagagcaagc ccaagatgta gcaagcagtc cacctgagag ctccttccag 1300  
aaactagcac ccagtgaata taggtatact ctattgaggg atcgagatga 1350  
gctttaaaaa cttgaaaaac agtttgtaag cctttcaaca gcagcatcaa 1400  
cctacgtggt ggaaatagta aacctatatt ttcataattc tatgtgtatt 1450  
tttattttga ataaacagaa agaaatttaa aaaaaaaaaa aaaaaaaaaa 1500  
aaaaaaaaaa aaaaaaaaaa aaa 1523

<210> 309  
<211> 406  
<212> PRT  
<213> Homo sapiens

<400> 309  
Met His Pro Ala Val Phe Leu Ser Leu Pro Asp Leu Arg Cys Ser  
1 5 10 15  
Leu Leu Leu Leu Val Thr Trp Val Phe Thr Pro Val Thr Thr Glu  
20 25 30  
Ile Thr Ser Leu Ala Thr Glu Asn Ile Asp Glu Ile Leu Asn Asn  
35 40 45  
Ala Asp Val Ala Leu Val Asn Phe Tyr Ala Asp Trp Cys Arg Phe  
50 55 60  
Ser Gln Met Leu His Pro Ile Phe Glu Glu Ala Ser Asp Val Ile  
65 70 75  
Lys Glu Glu Phe Pro Asn Glu Asn Gln Val Val Phe Ala Arg Val  
80 85 90  
Asp Cys Asp Gln His Ser Asp Ile Ala Gln Arg Tyr Arg Ile Ser  
95 100 105  
Lys Tyr Pro Thr Leu Lys Leu Phe Arg Asn Gly Met Met Met Lys  
110 115 120  
Arg Glu Tyr Arg Gly Gln Arg Ser Val Lys Ala Leu Ala Asp Tyr  
125 130 135  
Ile Arg Gln Gln Lys Ser Asp Pro Ile Gln Glu Ile Arg Asp Leu  
140 145 150  
Ala Glu Ile Thr Thr Leu Asp Arg Ser Lys Arg Asn Ile Ile Gly  
155 160 165  
Tyr Phe Glu Gln Lys Asp Ser Asp Asn Tyr Arg Val Phe Glu Arg  
170 175 180  
Val Ala Asn Ile Leu His Asp Asp Cys Ala Phe Leu Ser Ala Phe  
185 190 195

Gly	Asp	Val	Ser	Lys	Pro	Glu	Arg	Tyr	Ser	Gly	Asp	Asn	Ile	Ile	200	205	210
Tyr	Lys	Pro	Pro	Gly	His	Ser	Ala	Pro	Asp	Met	Val	Tyr	Leu	Gly	215	220	225
Ala	Met	Thr	Asn	Phe	Asp	Val	Thr	Tyr	Asn	Trp	Ile	Gln	Asp	Lys	230	235	240
Cys	Val	Pro	Leu	Val	Arg	Glu	Ile	Thr	Phe	Glu	Asn	Gly	Glu	Glu	245	250	255
Leu	Thr	Glu	Glu	Gly	Leu	Pro	Phe	Leu	Ile	Leu	Phe	His	Met	Lys	260	265	270
Glu	Asp	Thr	Glu	Ser	Leu	Glu	Ile	Phe	Gln	Asn	Glu	Val	Ala	Arg	275	280	285
Gln	Leu	Ile	Ser	Glu	Lys	Gly	Thr	Ile	Asn	Phe	Leu	His	Ala	Asp	290	295	300
Cys	Asp	Lys	Phe	Arg	His	Pro	Leu	Leu	His	Ile	Gln	Lys	Thr	Pro	305	310	315
Ala	Asp	Cys	Pro	Val	Ile	Ala	Ile	Asp	Ser	Phe	Arg	His	Met	Tyr	320	325	330
Val	Phe	Gly	Asp	Phe	Lys	Asp	Val	Leu	Ile	Pro	Gly	Lys	Leu	Lys	335	340	345
Gln	Phe	Val	Phe	Asp	Leu	His	Ser	Gly	Lys	Leu	His	Arg	Glu	Phe	350	355	360
His	His	Gly	Pro	Asp	Pro	Thr	Asp	Thr	Ala	Pro	Gly	Glu	Gln	Ala	365	370	375
Gln	Asp	Val	Ala	Ser	Ser	Pro	Pro	Glu	Ser	Ser	Phe	Gln	Lys	Leu	380	385	390
Ala	Pro	Ser	Glu	Tyr	Arg	Tyr	Thr	Leu	Leu	Arg	Asp	Arg	Asp	Glu	395	400	405

Leu

<210> 310  
 <211> 182  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 36, 48  
 <223> unknown base

<400> 310

attaaggaag aatttccaaa tgaaaatcaa gtagtntttg ccagagtnga 50  
ttgtgatcag cactctgaca tagcccagag atacaggata agcaaatacc 100  
caaccctcaa attgtttcgt aatgggatga tgatgaagag agaatacagg 150  
ggtcagcgat cagtgaaagc attggcagat ta 182

<210> 311

<211> 598

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 38, 59, 140, 169, 174, 183, 282-283, 294-295, 319, 396

<223> unknown base

<400> 311

agaggcctct ctggaagttg tcccgggtgt tcgccgcngg agcccgggtc 50  
gagaggacna ggtgccgctg cctggagaat cctccgctgc cgtcggctcc 100  
cggagcccag ccctttccta acccaacca acctagcccn gtcccagccg 150  
ccagcgcctg tocctgtcnc gganccagc gtnaccatgc atcctgccgt 200  
cttcctatcc ttacccgacc tcagatgctc cttctgctc ctggtaactt 250  
gggtttttac tcctgtaaca actgaaataa cnngtcttga tacnnagaat 300  
atagatgaaa ttttaaacna tgctgatgtg gctttagtca atttttatgc 350  
tgactgggtg cgtttcagtc agatgtggca tccaattttt gaggangctt 400  
ccgatgtcat taaggaagaa tttccaaatg aaaatcaagt agtgtttgcc 450  
agagttgatt gtgatcagca ctctgacata gccagagat acaggataag 500  
caaataccca accctcaaat tgtttcgtaa tgggatgatg atgaagagag 550  
aatacagggg tcagcgatca gtgaaagcat tggcagatta catcaggc 598

<210> 312

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 312

tgagaggcct ctctggaagt tg 22

<210> 313

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 313

gtcagcgatc agtgaaagc 19

<210> 314

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 314

ccagaatgaa gtagctcggc 20

<210> 315

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 315

ccgactcaaa atgcattgtc 20

<210> 316

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 316

catttggcag gaattgtcc 19

<210> 317

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 317

ggtgctatag gccaaagg 18

<210> 318

<211> 24

<212> DNA

<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 318  
ctgtatctct gggctatgtc agag 24

<210> 319  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 319  
ctacatataa tggcacatgt cagcc 25

<210> 320  
<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 320  
cgtcttctcta tccttaccgc acctcagatg ctcccttctg ctctg 46

<210> 321  
<211> 1333  
<212> DNA  
<213> Homo sapiens

<400> 321  
gcccacgcgt ccgatggcgt tcacgttcgc ggccttctgc tacatgctgg 50  
cgctgctgct cactgccgcg ctcatcttct tcgccatttg gcacattata 100  
gcatttgatg agctgaagac tgattacaag aatcctatag accagtgtaa 150  
taccctgaat ccccttgtag tcccagagta cctcatccac gctttcttct 200  
gtgtcatgtt tctttgtgca gcagagtggc ttacactggg tctcaatatg 250  
cccctcttgg catatcatat ttggaggtat atgagtagac cagtgatgag 300  
tggcccagga ctctatgacc ctacaaccat catgaatgca gataattctag 350  
catattgtca gaaggaagga tgggtgcaa tagcttttta tcttctagca 400  
tttttttact acctatatgg catgatctat gttttggtga gctcttagaa 450  
caacacacag aagaattggt ccagttaagt gcatgcaaaa agccaccaa 500  
tgaagggatt ctatccagca agatcctgtc caagagtagc ctgtggaatc 550  
tgatcagtta ctttaaaaaa tgactcctta ttttttaa gtttccacat 600



ttttgcttgt ggaaagactg ttttcatatg ttatactcag ataaagattt 650  
 taaatggtat tacgtataaa ttaatatata atgattacct ctggtgttga 700  
 caggtttgaa cttgcacttc ttaaggaaca gccataatcc tctgaatgat 750  
 gcattaatta ctgactgtcc tagtacattg gaagcttttg tttataggaa 800  
 cttgtagggc tcatttttggc ttcatgaaa cagtatctaa ttataaatta 850  
 gctgtagata tcagggtgctt ctgatgaagt gaaaatgtat atctgactag 900  
 tgggaaaactt catgggtttc ctcatctgtc atgtcgatga ttatatatgg 950  
 atacatttac aaaaataaaa agcgggaatt ttcccttcgc ttgaatatta 1000  
 tccctgtata ttgcatgaat gagagatttc ccatatttcc atcagagtaa 1050  
 taaatatact tgctttaatt cttaagcata agtaaacadg atataaaaat 1100  
 atatgctgaa ttacttgtga agaatgcatt taaagctatt ttaaagtgtg 1150  
 ttttatttgt aagacattac ttattaagaa attggttatt atgcttactg 1200  
 ttctaactcg gtggttaaagg tattcttaag aatttgcagg tactacagat 1250  
 tttcaaaaact gaatgagaga aaattgtata accatcctgc tgttccttta 1300  
 gtgcaataca ataaaactct gaaattaaga ctc 1333

<210> 322  
 <211> 144  
 <212> PRT  
 <213> Homo sapiens

<400> 322  
 Met Ala Phe Thr Phe Ala Ala Phe Cys Tyr Met Leu Ala Leu Leu  
 1 5 10 15  
 Leu Thr Ala Ala Leu Ile Phe Phe Ala Ile Trp His Ile Ile Ala  
 20 25 30  
 Phe Asp Glu Leu Lys Thr Asp Tyr Lys Asn Pro Ile Asp Gln Cys  
 35 40 45  
 Asn Thr Leu Asn Pro Leu Val Leu Pro Glu Tyr Leu Ile His Ala  
 50 55 60  
 Phe Phe Cys Val Met Phe Leu Cys Ala Ala Glu Trp Leu Thr Leu  
 65 70 75  
 Gly Leu Asn Met Pro Leu Leu Ala Tyr His Ile Trp Arg Tyr Met  
 80 85 90  
 Ser Arg Pro Val Met Ser Gly Pro Gly Leu Tyr Asp Pro Thr Thr  
 95 100 105

Ile Met Asn Ala Asp Ile Leu Ala Tyr Cys Gln Lys Glu Gly Trp  
110 115 120

Cys Lys Leu Ala Phe Tyr Leu Leu Ala Phe Phe Tyr Tyr Leu Tyr  
125 130 135

Gly Met Ile Tyr Val Leu Val Ser Ser  
140

<210> 323  
<211> 477  
<212> DNA  
<213> Homo sapiens

<400> 323  
attatagcat ttgatgagct gaagactgat tacaagatcc tatagaccag 50  
tgtaataccc tgaatcccct tgtactocca gagtacctca tccacgcttt 100  
cttctgtgtc atgtttcttt gtgcagcaga gtggcttaca ctgggtctca 150  
atatgccctt cttggcatat catatttggg ggtatatgag tagaccagtg 200  
atgagtggcc caggactcta tgaccctaca accatcatga atgcagatat 250  
tctagcatat tgtcagaagg aaggatgggtg caaattagct ttttatcttc 300  
tagcattttt ttactacctt tatggcatga tctatgtttt ggtgagctct 350  
tagaacaaca cacagaagaa ttggtccagt taagtgcatt caaaaagcca 400  
ccaaatgaag ggattctatc cagcaagatc ctgtccaaga gtagcctgtg 450  
gaatctgata agttacttta aaaaatg 477

<210> 324  
<211> 43  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 324  
tgtaaaacga cggccagttt aatagacctg caattattat tct 43

<210> 325  
<211> 41  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 325  
caggaaacag ctatgaccac ctgcacacct gcaaattcat t 41

<210> 326  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 326  
gtgcagcaga gtggcttaca 20

<210> 327  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 327  
actggaccaa ttcttctgtg 20

<210> 328  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 328  
gatattctag catattgtca gaaggaagga tggcgcaaat tagct 45

<210> 329  
<211> 1174  
<212> DNA  
<213> Homo sapiens

<400> 329  
cggacgcgtg ggggaaaccc ttccgagaaa acagcaacaa gctgagctgc 50  
tgtgacagag gggaacaaga tggcggcgcc gaaggggagc ctctgggtga 100  
ggacccaact ggggctcccg ccgctgctgc tgctgaccat ggccttggcc 150  
ggaggttcgg ggaccgcttc ggctgaagca ttgactcgg tcttggtga 200  
tacggcgtct tgccaccggg cctgtcagtt gacctacccc ttgcacacct 250  
accctaagga agaggagttg tacgcatgtc agagaggttg caggctgttt 300  
tcaatttgtc agtttgtgga tgatggaatt gacttaaadc gaactaaatt 350  
ggaatgtgaa tctgcatgta cagaagcata ttcccaatct gatgagcaat 400  
atgcttgcca tcttggttgc cagaatcagc tgccattcgc tgaactgaga 450

caagaacaac ttatgtccct gatgccaaaa atgcacctac tctttcctct 500  
 aactctgggtg aggtcattct ggagtgacat gatggactcc gcacagagct 550  
 tcataacctc ttcattggact ttttatcttc aagccgatga cggaaaaata 600  
 gttatattcc agtctaagcc agaaatccag tacgcaccac atttggagca 650  
 ggagcctaca aatttgagag aatcatctct aagcaaaatg tcctatctgc 700  
 aaatgagaaa ttcacaagcg cacaggaatt ttcttgaaga tggagaaagt 750  
 gatggctttt taagatgcct ctctcttaac tctgggtgga ttttaactac 800  
 aactcttgtc ctctcggtga tggatttgct ttggatttgt tgtgcaactg 850  
 ttgctacagc tgtggagcag tatgttcctt ctgagaagct gagtatctat 900  
 ggtgacttgg agtttatgaa tgaacaaaag ctaaacagat atccagcttc 950  
 ttctcttggtg gttgttagat ctaaaactga agatcatgaa gaagcagggc 1000  
 ctctacctac aaaagtgaat cttgctcatt ctgaaattta agcatttttc 1050  
 ttttaaaaga caagtgaat agacatctaa aattccactc ctcatagagc 1100  
 ttttaaaatg gtttcattgg atataggcct taagaaatca ctataaaatg 1150  
 caaataaagt tactcaaate tgtg 1174

<210> 330

<211> 323

<212> PRT

<213> Homo sapiens

<400> 330

Met	Ala	Ala	Pro	Lys	Gly	Ser	Leu	Trp	Val	Arg	Thr	Gln	Leu	Gly
1				5					10					15
Leu	Pro	Pro	Leu	Leu	Leu	Leu	Thr	Met	Ala	Leu	Ala	Gly	Gly	Ser
			20					25						30
Gly	Thr	Ala	Ser	Ala	Glu	Ala	Phe	Asp	Ser	Val	Leu	Gly	Asp	Thr
			35					40						45
Ala	Ser	Cys	His	Arg	Ala	Cys	Gln	Leu	Thr	Tyr	Pro	Leu	His	Thr
			50					55						60
Tyr	Pro	Lys	Glu	Glu	Glu	Leu	Tyr	Ala	Cys	Gln	Arg	Gly	Cys	Arg
			65					70						75
Leu	Phe	Ser	Ile	Cys	Gln	Phe	Val	Asp	Asp	Gly	Ile	Asp	Leu	Asn
			80					85						90
Arg	Thr	Lys	Leu	Glu	Cys	Glu	Ser	Ala	Cys	Thr	Glu	Ala	Tyr	Ser
			95					100						105

Gln Ser Asp Glu	Gln Tyr Ala Cys His	Leu Gly Cys Gln Asn Gln
110	115	120
Leu Pro Phe Ala	Glu Leu Arg Gln Glu	Gln Leu Met Ser Leu Met
125	130	135
Pro Lys Met His	Leu Leu Phe Pro Leu	Thr Leu Val Arg Ser Phe
140	145	150
Trp Ser Asp Met	Met Asp Ser Ala Gln	Ser Phe Ile Thr Ser Ser
155	160	165
Trp Thr Phe Tyr	Leu Gln Ala Asp Asp	Gly Lys Ile Val Ile Phe
170	175	180
Gln Ser Lys Pro	Glu Ile Gln Tyr Ala	Pro His Leu Glu Gln Glu
185	190	195
Pro Thr Asn Leu	Arg Glu Ser Ser Leu	Ser Lys Met Ser Tyr Leu
200	205	210
Gln Met Arg Asn	Ser Gln Ala His Arg	Asn Phe Leu Glu Asp Gly
215	220	225
Glu Ser Asp Gly	Phe Leu Arg Cys Leu	Ser Leu Asn Ser Gly Trp
230	235	240
Ile Leu Thr Thr	Thr Leu Val Leu Ser	Val Met Val Leu Leu Trp
245	250	255
Ile Cys Cys Ala	Thr Val Ala Thr Ala	Val Glu Gln Tyr Val Pro
260	265	270
Ser Glu Lys Leu	Ser Ile Tyr Gly Asp	Leu Glu Phe Met Asn Glu
275	280	285
Gln Lys Leu Asn	Arg Tyr Pro Ala Ser	Ser Leu Val Val Val Arg
290	295	300
Ser Lys Thr Glu	Asp His Glu Glu Ala	Gly Pro Leu Pro Thr Lys
305	310	315
Val Asn Leu Ala	His Ser Glu Ile	
320		

<210> 331  
 <211> 350  
 <212> DNA  
 <213> Homo sapiens

<400> 331  
 ttgggtgata cggcgtcttg ccaccggggc tgtcagttga cctaccctt 50  
 gcacacctac cctaaggaag aggagttgta cgcattgtcag agaggttgca 100  
 ggctgttttc aatttgtcag tttgtggatg atggaattga cttaaatacga 150

actaaattgg aatgtgaatc tgcattgtaca gaagcatatt cccaatctga 200  
tgagcaatat gcttgccatc ttggttgcca gaatcagctg ccattcgctg 250  
aactgagaca agaacaactt atgtccctga tgccaaaaat gcacctactc 300  
tttcctctaa ctctggtgag gtcattctgg agtgacatga tggactccgc 350

<210> 332  
<211> 562  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 47  
<223> unknown base

<400> 332  
cacactggcc ggatctttta gagtcctttg accttgacca agggctcngga 50  
aaacagcaac aagctgagct gctgtgacag agggaacaag atggcggcgc 100  
cgaaggagc ctttggtgga ggacccaact ggggctcccg ccgctgctgc 150  
tgctgaccat ggccttggcc ggagggttcgg ggaccgcttc ggctgaagca 200  
tttgactcgg tcttggtgga tacggcgtct tgccaccggg cctgtcagtt 250  
gacctacccc ttgcacacct accctaagga agaggagttg tacgcatgtc 300  
agagagggttg caggctgttt tcaatttgtc agtttgtgga tgatggaatt 350  
gacttaaadc gaactaaatt ggaatgtgaa tctgcatgta cagaagcata 400  
ttcccaatct gatgagcaat atgcttgcca tcttggttgc cagaatcagc 450  
tgccattcgc tgaactgaga caagaacaac ttatgtccct gatgccaaaa 500  
atgcacctac tctttcctct aactctggtg aggtcattct ggagtgcacat 550  
gatggactcc gc 562

<210> 333  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 333  
acaagctgag ctgctgtgac ag 22

<210> 334  
<211> 22

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 334  
tgattctggc aaccaagatg gc 22

<210> 335  
<211> 40  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 335  
atggccttgg ccggagggttc ggggaccgct tcggctgaag 40

<210> 336  
<211> 1885  
<212> DNA  
<213> Homo sapiens

<400> 336  
gcgagggtggc gatcgctgag aggcaggagg gccgaggcgg gcctgggagg 50  
cggcccggag gtggggcgcc gctggggccg gcccgcacgg gcttcatctg 100  
agggcgcacg gcccgcgacc gagcgtgcgg actggcctcc caagcgtggg 150  
gcgacaagct gccggagctg caatgggccc cggctgggga ttcttgtttg 200  
gcctcctggg cgccgtgtgg ctgctcagct cgggccacgg agaggagcag 250  
cccccggaga cagcggcaca gaggtgcttc tgccaggtta gtggttactt 300  
ggatgattgt acctgtgatg ttgaaacct tgatagattt aataactaca 350  
ggcttttccc aagactacaa aaacttcttg aaagtgacta ctttaggtat 400  
tacaaggtaa acctgaagag gccgtgtcct ttctggaatg acatcagcca 450  
gtgtggaaga agggactgtg ctgtcaaacc atgtcaatct gatgaagttc 500  
ctgatggaat taaatctgcg agctacaagt attctgaaga agccaataat 550  
ctcattgaag aatgtgaaca agctgaacga cttggagcag tggatgaatc 600  
tctgagtgag gaaacacaga aggctgttct tcagtggacc aagcatgatg 650  
attcttcaga taacttctgt gaagctgatg acattcagtc ccctgaagct 700  
gaatatgtag atttgcttct taatcctgag cgctacactg gttacaaggg 750  
accagatgct tggaaaatat ggaatgtcat ctacgaagaa aactgtttta 800

agccacagac aattaaaaga cctttaaatc ctttggttc tgggtcaagg 850  
 acaagtgaag agaacacttt ttacagttgg ctagaaggtc tctgtgtaga 900  
 aaaaagagca ttctacagac ttatatctgg cctacatgca agcattaatg 950  
 tgcatttgag tgcaagatat cttttacaag agacctggtt agaaaagaaa 1000  
 tggggacaca acattacaga atttcaacag cgatttgatg gaattttgac 1050  
 tgaaggagaa ggtccaagaa ggcttaagaa cttgtatttt ctctacttaa 1100  
 tagaactaag ggctttatcc aaagtgttac cattcttcga gcgcccagat 1150  
 tttcaactct ttactggaaa taaaattcag gatgaggaaa acaaaatggt 1200  
 acttctggaa atacttcatg aaatcaagtc atttcctttg cattttgatg 1250  
 agaattcatt ttttgctggg gataaaaaag aagcacacaa actaaaggag 1300  
 gactttcgac tgcattttag aaatatttca agaattatgg attgtgttgg 1350  
 ttgttttaaa tgcgtctgtt ggggaaagct tcagactcag ggtttgggca 1400  
 ctgctctgaa gatcttattt tctgagaaat tgatagcaaa tatgccagaa 1450  
 agtggaccta gttatgaatt ccatctaacc agacaagaaa tagtatcatt 1500  
 attcaacgca tttggaagaa tttctacaag tgtgaaagaa ttagaaaact 1550  
 tcaggaactt gttacagaat attcattaaa gaaaacaagc tgatatgtgc 1600  
 ctgtttctgg acaatggagg cgaaagagtg gaatttcatt caaaggcata 1650  
 atagcaatga cagtcttaag ccaaacattt tatataaagt tgcttttgta 1700  
 aaggagaatt atattgtttt aagtaaacac attttttaaa attgtgttaa 1750  
 gtctatgtat aatactactg tgagtaaaag taatacttta ataatgtggt 1800  
 acaaatttta aagtttaata ttgaataaaa ggaggattat caaattaaaa 1850  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 1885

<210> 337  
 <211> 468  
 <212> PRT  
 <213> Homo sapiens

<400> 337  
 Met Gly Arg Gly Trp Gly Phe Leu Phe Gly Leu Leu Gly Ala Val  
   1                  5                  10                  15  
 Trp Leu Leu Ser Ser Gly His Gly Glu Glu Gln Pro Pro Glu Thr  
                   20                  25                  30



Ala	Ala	Gln	Arg	Cys	Phe	Cys	Gln	Val	Ser	Gly	Tyr	Leu	Asp	Asp	35	40	45
Cys	Thr	Cys	Asp	Val	Glu	Thr	Ile	Asp	Arg	Phe	Asn	Asn	Tyr	Arg	50	55	60
Leu	Phe	Pro	Arg	Leu	Gln	Lys	Leu	Leu	Glu	Ser	Asp	Tyr	Phe	Arg	65	70	75
Tyr	Tyr	Lys	Val	Asn	Leu	Lys	Arg	Pro	Cys	Pro	Phe	Trp	Asn	Asp	80	85	90
Ile	Ser	Gln	Cys	Gly	Arg	Arg	Asp	Cys	Ala	Val	Lys	Pro	Cys	Gln	95	100	105
Ser	Asp	Glu	Val	Pro	Asp	Gly	Ile	Lys	Ser	Ala	Ser	Tyr	Lys	Tyr	110	115	120
Ser	Glu	Glu	Ala	Asn	Asn	Leu	Ile	Glu	Glu	Cys	Glu	Gln	Ala	Glu	125	130	135
Arg	Leu	Gly	Ala	Val	Asp	Glu	Ser	Leu	Ser	Glu	Glu	Thr	Gln	Lys	140	145	150
Ala	Val	Leu	Gln	Trp	Thr	Lys	His	Asp	Asp	Ser	Ser	Asp	Asn	Phe	155	160	165
Cys	Glu	Ala	Asp	Asp	Ile	Gln	Ser	Pro	Glu	Ala	Glu	Tyr	Val	Asp	170	175	180
Leu	Leu	Leu	Asn	Pro	Glu	Arg	Tyr	Thr	Gly	Tyr	Lys	Gly	Pro	Asp	185	190	195
Ala	Trp	Lys	Ile	Trp	Asn	Val	Ile	Tyr	Glu	Glu	Asn	Cys	Phe	Lys	200	205	210
Pro	Gln	Thr	Ile	Lys	Arg	Pro	Leu	Asn	Pro	Leu	Ala	Ser	Gly	Gln	215	220	225
Gly	Thr	Ser	Glu	Glu	Asn	Thr	Phe	Tyr	Ser	Trp	Leu	Glu	Gly	Leu	230	235	240
Cys	Val	Glu	Lys	Arg	Ala	Phe	Tyr	Arg	Leu	Ile	Ser	Gly	Leu	His	245	250	255
Ala	Ser	Ile	Asn	Val	His	Leu	Ser	Ala	Arg	Tyr	Leu	Leu	Gln	Glu	260	265	270
Thr	Trp	Leu	Glu	Lys	Lys	Trp	Gly	His	Asn	Ile	Thr	Glu	Phe	Gln	275	280	285
Gln	Arg	Phe	Asp	Gly	Ile	Leu	Thr	Glu	Gly	Glu	Gly	Pro	Arg	Arg	290	295	300
Leu	Lys	Asn	Leu	Tyr	Phe	Leu	Tyr	Leu	Ile	Glu	Leu	Arg	Ala	Leu	305	310	315

Ser	Lys	Val	Leu	Pro	Phe	Phe	Glu	Arg	Pro	Asp	Phe	Gln	Leu	Phe	320	325	330
Thr	Gly	Asn	Lys	Ile	Gln	Asp	Glu	Glu	Asn	Lys	Met	Leu	Leu	Leu	335	340	345
Glu	Ile	Leu	His	Glu	Ile	Lys	Ser	Phe	Pro	Leu	His	Phe	Asp	Glu	350	355	360
Asn	Ser	Phe	Phe	Ala	Gly	Asp	Lys	Lys	Glu	Ala	His	Lys	Leu	Lys	365	370	375
Glu	Asp	Phe	Arg	Leu	His	Phe	Arg	Asn	Ile	Ser	Arg	Ile	Met	Asp	380	385	390
Cys	Val	Gly	Cys	Phe	Lys	Cys	Arg	Leu	Trp	Gly	Lys	Leu	Gln	Thr	395	400	405
Gln	Gly	Leu	Gly	Thr	Ala	Leu	Lys	Ile	Leu	Phe	Ser	Glu	Lys	Leu	410	415	420
Ile	Ala	Asn	Met	Pro	Glu	Ser	Gly	Pro	Ser	Tyr	Glu	Phe	His	Leu	425	430	435
Thr	Arg	Gln	Glu	Ile	Val	Ser	Leu	Phe	Asn	Ala	Phe	Gly	Arg	Ile	440	445	450
Ser	Thr	Ser	Val	Lys	Glu	Leu	Glu	Asn	Phe	Arg	Asn	Leu	Leu	Gln	455	460	465

Asn Ile His

<210> 338  
 <211> 507  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 101, 263, 376, 397, 426  
 <223> unknown base

<400> 338  
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 ttaaaagacc tttaaactct ttggcttctg gtcaaggac aagtgaagag 100  
 nacacttttt acagttggct agaaggctc tgtgtagaaa aaagagcatt 150  
 ctacagactt atatctggcc tacatgcaag cattaatgtg catttgagtg 200  
 caagatatct ttacaagag acctggtag aaaagaaatg gggacacaac 250  
 attacagaat ttnaacagcg atttgatgga attttgactg aaggagaagg 300  
 tccaagaagg cttaagaact tgtattttct ctacttaata gaactaaggg 350

ctttatccaa agtgttacca ttcttngagc gcccagattt tcaactnttt 400  
actggaaata aaattcagga tgaggnaaac aaaatgttac ttttggaat 450  
acttcatgaa atcaagtcac ttcttttgca ttttgatgag aattcatttt 500  
tttgctg 507

<210> 339  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 339  
aagctgccgg agctgcaatg 20

<210> 340  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 340  
ttgcttctta atcctgagcg c 21

<210> 341  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 341  
aaaggaggac tttcgactgc 20

<210> 342  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 342  
agagattcat ccactgctcc aagtcg 26

<210> 343  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 343  
tgtccagaaa caggcacata tcagc 25

<210> 344  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 344  
agacagcggc acagaggtgc ttctgccagg ttagtggtta cttggatgat 50

<210> 345  
<211> 1486  
<212> DNA  
<213> Homo sapiens

<400> 345  
cggacgcgtg ggcggacgcg tgggcggacg cgtgggttgg gagggggcag 50  
gatgggaggg aaagtgaaga aaacagaaaa ggagagggac agaggccaga 100  
ggactttctca tactggacag aaaccgatca ggcattggaac tccccttcgt 150  
cactcacctg ttcttgcccc tgggtgttct gacaggtctc tgctccccct 200  
ttaacctgga tgaacatcac ccacgcctat tcccagggcc accagaagct 250  
gaatttgat acagtgtctt acaacatgtt gggggtggac agcgatggat 300  
gctggtgggc gccccctggg atgggccttc aggcgaccgg aggggggacg 350  
tttatcgctg ccctgtaggg gggggcccaca atgccccatg tgccaagggc 400  
cacttaggtg actaccaact gggaaattca tctcatctg ctgtgaatat 450  
gcacctgggg atgtctctgt tagagacaga tggatgatgg ggattcatgg 500  
tgagctaagg agagggtggt ggcagtgtct ctgaagggtcc ataaaagaaa 550  
aaagagaagt gtggttaaggg aaaatggtct gtgtggaggg gtcaaggagt 600  
taaaaaccct agaaagcaaa aggtaggtaa tgtcaggag tagtcttcat 650  
gcctccttca actgggagca tgttctgagg gtgccctccc aagcctggga 700  
gtaactatit ccccatccc caggcctgtg cccctctctg gtctcgtgct 750  
tgtggcagct ctgtcttcag ttctgggata tgtgcccggt tggatgcttc 800  
attccagcct cagggaagcc tggcaccac tgcccaacgt gagccagagg 850

aaggctgagt acttggttcc cagaaggaga tactgggtgg gaaaaagatg 900  
gggcaaagcg gtatgatgcc tggcaaaggg cctgcatggc tatectcatt 950  
gctacctaata gtgcttgcaa aagctccatg tttcctaaca gattcagact 1000  
cctggccagg tgtggtggcc cacacctgta attctagcac tttgggaggc 1050  
caagggtgggc agatcacttg aggtcaggag ttcaagacca gcctggccaa 1100  
catggtgaaa ctccatctct actaaaaaaaa aaaaaataca aaaattagct 1150  
gggtgcgcta gtgcatgcct gtaatctcat ctactcggga ggctaagaca 1200  
ggagactctc acttcaaccc aggaggtgga gggtgcggtg agccaagatt 1250  
gtgcctctgc actctagcgt gggtgacaga gtaagcgaga ctccatctca 1300  
aaaataataa taataataat tcagactcct tatcaggagt ccatgatctg 1350  
gcctggcaca gtaactcatg cctgtaatcc caacattttg ggaggccaac 1400  
gcaggaggat tgcttgaggt ctggagggtt gagaccagcc tgggcaacat 1450  
agaaagaccc catctctaaa taaatgtttt aaaaat 1486

<210> 346

<211> 124

<212> PRT

<213> Homo sapiens

<400> 346

Met	Glu	Leu	Pro	Phe	Val	Thr	His	Leu	Phe	Leu	Pro	Leu	Val	Phe
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Leu	Thr	Gly	Leu	Cys	Ser	Pro	Phe	Asn	Leu	Asp	Glu	His	His	Pro
				20					25					30
Arg	Leu	Phe	Pro	Gly	Pro	Pro	Glu	Ala	Glu	Phe	Gly	Tyr	Ser	Val
				35					40					45
Leu	Gln	His	Val	Gly	Gly	Gly	Gln	Arg	Trp	Met	Leu	Val	Gly	Ala
				50					55					60
Pro	Trp	Asp	Gly	Pro	Ser	Gly	Asp	Arg	Arg	Gly	Asp	Val	Tyr	Arg
				65					70					75
Cys	Pro	Val	Gly	Gly	Ala	His	Asn	Ala	Pro	Cys	Ala	Lys	Gly	His
				80					85					90
Leu	Gly	Asp	Tyr	Gln	Leu	Gly	Asn	Ser	Ser	His	Pro	Ala	Val	Asn
				95					100					105
Met	His	Leu	Gly	Met	Ser	Leu	Leu	Glu	Thr	Asp	Gly	Asp	Gly	Gly
				110					115					120

Phe Met Val Ser

<210> 347  
<211> 509  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 22  
<223> unknown base

<400> 347  
cacagttccc caccatcact cntcccatc cttccaactt tatttttagc 50  
ttgccattgg gagggggcag gatgggaggg aaagtgaaga aaacagaaaa 100  
ggagaggggac agaggccaga ggactttctca tactggacag aaaccgatca 150  
ggcatggaac tccccttcgt cactcacctg ttcttgcccc tgggtgttct 200  
gacaggtctc tgctccccct ttaacctgga tgaacatcac ccacgcctat 250  
tcccagggcc accagaagct gaatttgat acagtgtctt acaacatgtt 300  
gggggtggac agcgatggat gctggtgggc gccccctggg atgggccttc 350  
aggcgaccgg aggggggacg tttatcgctg ccctgtaggg gggggccaca 400  
atgccccatg tgccaagggc cacttaggtg actaccaact gggaaattca 450  
tctcatcctg ctgtgaatat gcacctgggg atgtctctgt tagagacaga 500  
tggatgatgg 509

<210> 348  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 348  
agggacagag gccagaggac ttc 23

<210> 349  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 349  
caggtgcata ttcacagcag gatg 24

<210> 350  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 350  
ggaactcccc ttcgctactc acctgttctt gcccctggtg ttcct 45

<210> 351  
<211> 2056  
<212> DNA  
<213> Homo sapiens

<400> 351  
aaagttacat tttctctgga actctcctag gccactccct gctgatgcaa 50  
catctggggt tgggcagaaa ggaggggtgct tcggagcccg ccctttctga 100  
gcttcctggg ccggtctctag aacaattcag gcttcgctgc gactcagacc 150  
tcagctccaa catatgcatt ctgaagaaag atggctgaga tggacagaat 200  
gctttatattt ggaaagaaac aatgttctag gtcaaactga gtctaccaa 250  
tgcagacttt cacaatgggt ctagaagaaa tctggacaag tcttttcatg 300  
tgggttttct acgcattgat tccatgtttg ctcacagatg aagtggccat 350  
tctgcctgcc cctcagaacc tctctgtact ctcaaccaac atgaagcatc 400  
tcttgatgtg gagcccagtg atcgcgctg gagaaacagt gtactattct 450  
gtcgaatacc agggggagta cgagagcctg tacacgagcc acatctggat 500  
cccagcagc tgggtgctcac tcaactgaagg tcctgagtgt gatgtcactg 550  
atgacatcac ggccactgtg ccatacaacc ttcgtgtcag ggccacattg 600  
ggctcacaga cctcagcctg gagcatcctg aagcatccct ttaatagaaa 650  
ctcaaccatc cttacccgac ctgggatgga gatcaccaaa gatggcttcc 700  
acctggttat tgagctggag gacctggggc ccagtttga gttccttgtg 750  
gcctactgga ggagggagcc tggtgccgag gaacatgtca aaatggtgag 800  
gagtgggggt attccagtgc acctagaaac catggagcca ggggctgcat 850  
actgtgtgaa ggcccagaca ttcgtgaagg ccattgggag gtacagcgcc 900  
ttcagccaga cagaatgtgt ggaggtgcaa ggagaggcca ttcccctggt 950  
actggccctg tttgcctttg ttggcttcat gctgacctt gtggctgtgc 1000

cactgttcgt ctggaaaatg ggccggctgc tccagtactc ctggtgcccc 1050  
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 aatcagctgc agaagggagg aggtggatgc ctgtgccacg gctgtgatgt 1150  
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 caggtgaagc cgagaacctg gtctgcatga catggaaacc atgaggggac 1250  
 aagttgtgtt tctgttttcc gccacggaca agggatgaga gaagtaggaa 1300  
 gagcctgttg tctacaagtc tagaagcaac catcagaggc aggggtggtt 1350  
 gtctaacaga aactgactg aggcctaggg gatgtgacct ctagactggg 1400  
 ggctgccact tgctggctga gcaaccctgg gaaaagtgac ttcattccctt 1450  
 cggtcctaag ttttctcatc tgtaatgggg gaattaccta cacacctgct 1500  
 aaacacacac acacagagtc tctctctata tatacacacg tacacataaa 1550  
 tacaccagc acttgcaagg ctagaggga aactggtgaca ctctacagtc 1600  
 tgactgattc agtgtttctg gagagcagga cataaatgta tgatgagaat 1650  
 gatcaaggac tctacacact ggggtggcttg gagagcccac tttcccagaa 1700  
 taatccttga gagaaaagga atcatgggag caatggtgtt gagttcactt 1750  
 caagcccaat gccggtgcag aggggaatgg cttagcgagc tctacagtag 1800  
 gtgacctgga ggaaggtcac agccacactg aaaatgggat gtgcatgaac 1850  
 acggaggatc catgaactac tgtaaagtgt tgacagtgtg tgcacactgc 1900  
 agacagcagg tgaaatgtat gtgtgcaatg cgacgagaat gcagaagtca 1950  
 gtaacatgtg catgtttgtt gtgctccttt tttctgttgg taaagtacag 2000  
 aattcagcaa ataaaaaggg ccaccctggc caaaagcggg aaaaaaaaaa 2050  
 aaaaaa 2056

<210> 352

<211> 311

<212> PRT

<213> Homo sapiens

<400> 352

Met	Gln	Thr	Phe	Thr	Met	Val	Leu	Glu	Glu	Ile	Trp	Thr	Ser	Leu
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Phe	Met	Trp	Phe	Phe	Tyr	Ala	Leu	Ile	Pro	Cys	Leu	Leu	Thr	Asp
			20					25					30	



Glu	Val	Ala	Ile	Leu	Pro	Ala	Pro	Gln	Asn	Leu	Ser	Val	Leu	Ser	35	40	45
Thr	Asn	Met	Lys	His	Leu	Leu	Met	Trp	Ser	Pro	Val	Ile	Ala	Pro	50	55	60
Gly	Glu	Thr	Val	Tyr	Tyr	Ser	Val	Glu	Tyr	Gln	Gly	Glu	Tyr	Glu	65	70	75
Ser	Leu	Tyr	Thr	Ser	His	Ile	Trp	Ile	Pro	Ser	Ser	Trp	Cys	Ser	80	85	90
Leu	Thr	Glu	Gly	Pro	Glu	Cys	Asp	Val	Thr	Asp	Asp	Ile	Thr	Ala	95	100	105
Thr	Val	Pro	Tyr	Asn	Leu	Arg	Val	Arg	Ala	Thr	Leu	Gly	Ser	Gln	110	115	120
Thr	Ser	Ala	Trp	Ser	Ile	Leu	Lys	His	Pro	Phe	Asn	Arg	Asn	Ser	125	130	135
Thr	Ile	Leu	Thr	Arg	Pro	Gly	Met	Glu	Ile	Thr	Lys	Asp	Gly	Phe	140	145	150
His	Leu	Val	Ile	Glu	Leu	Glu	Asp	Leu	Gly	Pro	Gln	Phe	Glu	Phe	155	160	165
Leu	Val	Ala	Tyr	Trp	Arg	Arg	Glu	Pro	Gly	Ala	Glu	Glu	His	Val	170	175	180
Lys	Met	Val	Arg	Ser	Gly	Gly	Ile	Pro	Val	His	Leu	Glu	Thr	Met	185	190	195
Glu	Pro	Gly	Ala	Ala	Tyr	Cys	Val	Lys	Ala	Gln	Thr	Phe	Val	Lys	200	205	210
Ala	Ile	Gly	Arg	Tyr	Ser	Ala	Phe	Ser	Gln	Thr	Glu	Cys	Val	Glu	215	220	225
Val	Gln	Gly	Glu	Ala	Ile	Pro	Leu	Val	Leu	Ala	Leu	Phe	Ala	Phe	230	235	240
Val	Gly	Phe	Met	Leu	Ile	Leu	Val	Val	Val	Pro	Leu	Phe	Val	Trp	245	250	255
Lys	Met	Gly	Arg	Leu	Leu	Gln	Tyr	Ser	Cys	Cys	Pro	Val	Val	Val	260	265	270
Leu	Pro	Asp	Thr	Leu	Lys	Ile	Thr	Asn	Ser	Pro	Gln	Lys	Leu	Ile	275	280	285
Ser	Cys	Arg	Arg	Glu	Glu	Val	Asp	Ala	Cys	Ala	Thr	Ala	Val	Met	290	295	300
Ser	Pro	Glu	Glu	Leu	Leu	Arg	Ala	Trp	Ile	Ser					305	310	

<210> 353  
<211> 864  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 654, 711, 748, 827  
<223> unknown base

<400> 353  
tcctgctgat gcacatctgg gtttggcaaa aggagggtgc ttcgagccgc 50  
cctttctagc ttcttgcccg gctctagaac aattcaggct tcgctgcgac 100  
tagacctcag ctccaacata tgcattctga agaaagatgg ctgagatgac 150  
agaatgcttt attttggaaa gaaacaatgt tctaggtcaa actgagtcta 200  
ccaaatgcag actttcacia tggttctaga agaaatctgg acaagtcttt 250  
tcatgtggtt tttctacgca ttgattccat gtttgctcac agatgaagtg 300  
gccattctgc ctgcccctca gaacctctct gtactctcaa ccaacatgaa 350  
gcatctcttg atgtggagcc cagtgatcgc gcctggagaa acagtgtact 400  
attctgtcga ataccagggg gagtacgaga gcctgtacac gagccacatc 450  
tggatcccca gcagctggtg ctcaactcact gaaggctctg agtgtgatgt 500  
cactgatgac atcacggcca ctgtgccata caacctttgt gtcagggcca 550  
cattgggctc acagacctca gcctggagca tcctgaagca tccctttaat 600  
agaaactcaa ccatacttac ccgacctggg atggagatca ccaaagatgg 650  
cttncacctg gttattgagc tggaggacct ggggccccag tttgagttcc 700  
ttgtggccta ntggaggagg ggcgaacccc ttgcggcgca aggggttngc 750  
gaaccccttg cggccgctgg ggtatctctc gagaaaagag aggcccaata 800  
tgaccacat actcaatatg gacgaantgc tattgtccac ctgtttgagt 850  
ggcgctgggt tgat 864

<210> 354  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 354  
aggcttcgct gcgactagac ctc 23

<210> 355  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 355  
ccaggtcggg taaggatggt tgag 24

<210> 356  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 356  
tttctacgca ttgattccat gtttgctcac agatgaagtg gccattctgc 50

<210> 357  
<211> 1670  
<212> DNA  
<213> Homo sapiens

<400> 357  
cccacgcgtc cgcccacgcg tccgagggac aagagagaag agagactgaa 50  
acagggagaa gaggcaggag aggaggaggt ggggagagca cgaagctgga 100  
ggccgacact gagggagggc gggaggaggt gaagaaggag agaggggaga 150  
agaggcagga gctggaaagg agagagggag gaggaggagg agatgcggga 200  
tgagacactg gagttaggtg gcttgggaga gcttaatgaa aagagaacgg 250  
agaggaggtg tgggttagga accaagaggt agccctgtgg gcagcagaag 300  
gctgagagga gtaggaagat caggagctag agggagactg gagggttccg 350  
ggaaaagagc agaggaaaga ggaaagacac agagagacgg gagagagaag 400  
aagagtgggt ttgaagggcg gatctcagtc cctggctgct ttggcatttg 450  
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<210> 358

<211> 328

<212> PRT

<213> Homo sapiens

<400> 358

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Trp	Ala	Ala	Leu	Gly	Ala	Ala	Ala	His	Ile	Gly	Pro	Ala	Pro	Asp
			20					25						30

Pro	Glu	Asp	Trp	Trp	Ser	Tyr	Lys	Asp	Asn	Leu	Gln	Gly	Asn	Phe
			35					40						45

Val	Pro	Gly	Pro	Pro	Phe	Trp	Gly	Leu	Val	Asn	Ala	Ala	Trp	Ser
					50			55						60

Leu	Cys	Ala	Val	Gly	Lys	Arg	Gln	Ser	Pro	Val	Asp	Val	Glu	Leu	65	70	75
Lys	Arg	Val	Leu	Tyr	Asp	Pro	Phe	Leu	Pro	Pro	Leu	Arg	Leu	Ser	80	85	90
Thr	Gly	Gly	Glu	Lys	Leu	Arg	Gly	Thr	Leu	Tyr	Asn	Thr	Gly	Arg	95	100	105
His	Val	Ser	Phe	Leu	Pro	Ala	Pro	Arg	Pro	Val	Val	Asn	Val	Ser	110	115	120
Gly	Gly	Pro	Leu	Leu	Tyr	Ser	His	Arg	Leu	Ser	Glu	Leu	Arg	Leu	125	130	135
Leu	Phe	Gly	Ala	Arg	Asp	Gly	Ala	Gly	Ser	Glu	His	Gln	Ile	Asn	140	145	150
His	Gln	Gly	Phe	Ser	Ala	Glu	Val	Gln	Leu	Ile	His	Phe	Asn	Gln	155	160	165
Glu	Leu	Tyr	Gly	Asn	Phe	Ser	Ala	Ala	Ser	Arg	Gly	Pro	Asn	Gly	170	175	180
Leu	Ala	Ile	Leu	Ser	Leu	Phe	Val	Asn	Val	Ala	Ser	Thr	Ser	Asn	185	190	195
Pro	Phe	Leu	Ser	Arg	Leu	Leu	Asn	Arg	Asp	Thr	Ile	Thr	Arg	Ile	200	205	210
Ser	Tyr	Lys	Asn	Asp	Ala	Tyr	Phe	Leu	Gln	Asp	Leu	Ser	Leu	Glu	215	220	225
Leu	Leu	Phe	Pro	Glu	Ser	Phe	Gly	Phe	Ile	Thr	Tyr	Gln	Gly	Ser	230	235	240
Leu	Ser	Thr	Pro	Pro	Cys	Ser	Glu	Thr	Val	Thr	Trp	Ile	Leu	Ile	245	250	255
Asp	Arg	Ala	Leu	Asn	Ile	Thr	Ser	Leu	Gln	Met	His	Ser	Leu	Arg	260	265	270
Leu	Leu	Ser	Gln	Asn	Pro	Pro	Ser	Gln	Ile	Phe	Gln	Ser	Leu	Ser	275	280	285
Gly	Asn	Ser	Arg	Pro	Leu	Gln	Pro	Leu	Ala	His	Arg	Ala	Leu	Arg	290	295	300
Gly	Asn	Arg	Asp	Pro	Arg	His	Pro	Glu	Arg	Arg	Cys	Arg	Gly	Pro	305	310	315
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<210> 359

<211> 24

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 359  
tctgctgagg tgcagctcat tcac 24

<210> 360  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 360  
gaggctctgg aagatctgag atgg 24

<210> 361  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 361  
gcctctttgt caacgttgcc agtacctota acccattcct cagtcgcctc 50

<210> 362  
<211> 3038  
<212> DNA  
<213> Homo sapiens

<400> 362  
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taaacattaa aattaatcat gtttcaaaaa aaaaaaaa 3038

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<210> 363
<211> 500
<212> PRT
<213> Homo sapiens

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<400> 363
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Phe Met Ala Arg Ala Ile Pro Ala Met Val Val Pro Asn Ala Thr
      20             25             30

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Leu	Leu	Glu	Lys	Leu	Leu	Glu	Lys	Tyr	Met	Asp	Glu	Asp	Gly	Glu			
				35					40					45			
Trp	Trp	Ile	Ala	Lys	Gln	Arg	Gly	Lys	Arg	Ala	Ile	Thr	Asp	Asn			
				50					55					60			
Asp	Met	Gln	Ser	Ile	Leu	Asp	Leu	His	Asn	Lys	Leu	Arg	Ser	Gln			
				65					70					75			
Val	Tyr	Pro	Thr	Ala	Ser	Asn	Met	Glu	Tyr	Met	Thr	Trp	Asp	Val			
				80					85					90			
Glu	Leu	Glu	Arg	Ser	Ala	Glu	Ser	Trp	Ala	Glu	Ser	Cys	Leu	Trp			
				95					100					105			
Glu	His	Gly	Pro	Ala	Ser	Leu	Leu	Pro	Ser	Ile	Gly	Gln	Asn	Leu			
				110					115					120			
Gly	Ala	His	Trp	Gly	Arg	Tyr	Arg	Pro	Pro	Thr	Phe	His	Val	Gln			
				125					130					135			
Ser	Trp	Tyr	Asp	Glu	Val	Lys	Asp	Phe	Ser	Tyr	Pro	Tyr	Glu	His			
				140					145					150			
Glu	Cys	Asn	Pro	Tyr	Cys	Pro	Phe	Arg	Cys	Ser	Gly	Pro	Val	Cys			
				155					160					165			
Thr	His	Tyr	Thr	Gln	Val	Val	Trp	Ala	Thr	Ser	Asn	Arg	Ile	Gly			
				170					175					180			
Cys	Ala	Ile	Asn	Leu	Cys	His	Asn	Met	Asn	Ile	Trp	Gly	Gln	Ile			
				185					190					195			
Trp	Pro	Lys	Ala	Val	Tyr	Leu	Val	Cys	Asn	Tyr	Ser	Pro	Lys	Gly			
				200					205					210			
Asn	Trp	Trp	Gly	His	Ala	Pro	Tyr	Lys	His	Gly	Arg	Pro	Cys	Ser			
				215					220					225			
Ala	Cys	Pro	Pro	Ser	Phe	Gly	Gly	Gly	Cys	Arg	Glu	Asn	Leu	Cys			
				230					235					240			
Tyr	Lys	Glu	Gly	Ser	Asp	Arg	Tyr	Tyr	Pro	Pro	Arg	Glu	Glu	Glu			
				245					250					255			
Thr	Asn	Glu	Ile	Glu	Arg	Gln	Gln	Ser	Gln	Val	His	Asp	Thr	His			
				260					265					270			
Val	Arg	Thr	Arg	Ser	Asp	Asp	Ser	Ser	Arg	Asn	Glu	Val	Ile	Ser			
				275					280					285			
Ala	Gln	Gln	Met	Ser	Gln	Ile	Val	Ser	Cys	Glu	Val	Arg	Leu	Arg			
				290					295					300			
Asp	Gln	Cys	Lys	Gly	Thr	Thr	Cys	Asn	Arg	Tyr	Glu	Cys	Pro	Ala			
				305					310					315			

Gly Cys Leu Asp Ser Lys Ala Lys Val Ile Gly Ser Val His Tyr	320	325	330
Glu Met Gln Ser Ser Ile Cys Arg Ala Ala Ile His Tyr Gly Ile	335	340	345
Ile Asp Asn Asp Gly Gly Trp Val Asp Ile Thr Arg Gln Gly Arg	350	355	360
Lys His Tyr Phe Ile Lys Ser Asn Arg Asn Gly Ile Gln Thr Ile	365	370	375
Gly Lys Tyr Gln Ser Ala Asn Ser Phe Thr Val Ser Lys Val Thr	380	385	390
Val Gln Ala Val Thr Cys Glu Thr Thr Val Glu Gln Leu Cys Pro	395	400	405
Phe His Lys Pro Ala Ser His Cys Pro Arg Val Tyr Cys Pro Arg	410	415	420
Asn Cys Met Gln Ala Asn Pro His Tyr Ala Arg Val Ile Gly Thr	425	430	435
Arg Val Tyr Ser Asp Leu Ser Ser Ile Cys Arg Ala Ala Val His	440	445	450
Ala Gly Val Val Arg Asn His Gly Gly Tyr Val Asp Val Met Pro	455	460	465
Val Asp Lys Arg Lys Thr Tyr Ile Ala Ser Phe Gln Asn Gly Ile	470	475	480
Phe Ser Glu Ser Leu Gln Asn Pro Pro Gly Gly Lys Ala Phe Arg	485	490	495
Val Phe Ala Val Val	500		

<210> 364

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 364

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<210> 365

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 365  
ccaagagtat actgtcctcg 20

<210> 366  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 366  
agcacagatt ttctctacag ccccc 25

<210> 367  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 367  
aaccactcca gcatgtactg ctgc 24

<210> 368  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 368  
ccattcaggt gttctggccc tgtatgtaca cattatacac aggtcgtgtg 50

<210> 369  
<211> 1685  
<212> DNA  
<213> Homo sapiens

<400> 369  
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<210> 370

<211> 111

<212> PRT

<213> Homo sapiens

<400> 370

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				20				25						30	
Arg	Val	Asp	Gly	Ser	Lys	Cys	Lys	Cys	Ser	Arg	Lys	Gly	Pro	Lys	
				35				40						45	
Ile	Arg	Tyr	Ser	Asp	Val	Lys	Lys	Leu	Glu	Met	Lys	Pro	Lys	Tyr	
				50				55						60	
Pro	His	Cys	Glu	Glu	Lys	Met	Val	Ile	Ile	Thr	Thr	Lys	Ser	Val	
				65				70						75	
Ser	Arg	Tyr	Arg	Gly	Gln	Glu	His	Cys	Leu	His	Pro	Lys	Leu	Gln	
				80				85						90	
Ser	Thr	Lys	Arg	Phe	Ile	Lys	Trp	Tyr	Asn	Ala	Trp	Asn	Glu	Lys	
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				110											

<210> 371

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 371

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<210> 372

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 372

tcccaactgg tttggagttt tccc 24

<210> 373

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 373

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<210> 374

<211> 3113

<212> DNA

<213> Homo sapiens

<400> 374

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<212> PRT

<213> Homo sapiens

<400> 375

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Thr	Asn	Tyr	Gly	Lys	Ile	Arg	Gly	Leu	Arg	Thr	Pro	Leu	Pro	Asn
				35					40					45
Glu	Ile	Leu	Gly	Pro	Val	Glu	Gln	Tyr	Leu	Gly	Val	Pro	Tyr	Ala
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Ser	Pro	Pro	Thr	Gly	Glu	Arg	Arg	Phe	Gln	Pro	Pro	Glu	Pro	Pro
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Ser	Ser	Trp	Thr	Gly	Ile	Arg	Asn	Thr	Thr	Gln	Phe	Ala	Ala	Val
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Cys	Pro	Gln	His	Leu	Asp	Glu	Arg	Ser	Leu	Leu	His	Asp	Met	Leu
				95					100					105
Pro	Ile	Trp	Phe	Thr	Ala	Asn	Leu	Asp	Thr	Leu	Met	Thr	Tyr	Val
				110					115					120
Gln	Asp	Gln	Asn	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Ile	Tyr	Val	Pro
				125					130					135
Thr	Glu	Asp	Gly	Ala	Asn	Thr	Lys	Lys	Asn	Ala	Asp	Asp	Ile	Thr
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Ser Asn Asp Arg	Gly Glu Asp Glu Asp	Ile His Asp Gln Asn Ser
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Lys Lys Pro Val	Met Val Tyr Ile His	Gly Gly Ser Tyr Met Glu
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Gly Thr Gly Asn	Met Ile Asp Gly Ser	Ile Leu Ala Ser Tyr Gly
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Asn Val Ile Val	Ile Thr Ile Asn Tyr	Arg Leu Gly Ile Leu Gly
200	205	210
Phe Leu Ser Thr	Gly Asp Gln Ala Ala	Lys Gly Asn Tyr Gly Leu
215	220	225
Leu Asp Gln Ile	Gln Ala Leu Arg Trp	Ile Glu Glu Asn Val Gly
230	235	240
Ala Phe Gly Gly	Asp Pro Lys Arg Val	Thr Ile Phe Gly Ser Gly
245	250	255
Ala Gly Ala Ser	Cys Val Ser Leu Leu	Thr Leu Ser His Tyr Ser
260	265	270
Glu Gly Leu Phe	Gln Lys Ala Ile Ile	Gln Ser Gly Thr Ala Leu
275	280	285
Ser Ser Trp Ala	Val Asn Tyr Gln Pro	Ala Lys Tyr Thr Arg Ile
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Leu Ala Asp Lys	Val Gly Cys Asn Met	Leu Asp Thr Thr Asp Met
305	310	315
Val Glu Cys Leu	Arg Asn Lys Asn Tyr	Lys Glu Leu Ile Gln Gln
320	325	330
Thr Ile Thr Pro	Ala Thr Tyr His Ile	Ala Phe Gly Pro Val Ile
335	340	345
Asp Gly Asp Val	Ile Pro Asp Asp Pro	Gln Ile Leu Met Glu Gln
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Gly Glu Phe Leu	Asn Tyr Asp Ile Met	Leu Gly Val Asn Gln Gly
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Glu Gly Leu Lys	Phe Val Asp Gly Ile	Val Asp Asn Glu Asp Gly
380	385	390
Val Thr Pro Asn	Asp Phe Asp Phe Ser	Val Ser Asn Phe Val Asp
395	400	405
Asn Leu Tyr Gly	Tyr Pro Glu Gly Lys	Asp Thr Leu Arg Glu Thr
410	415	420
Ile Lys Phe Met	Tyr Thr Asp Trp Ala	Asp Lys Glu Asn Pro Glu
425	430	435

Thr Arg Arg Lys	Thr Leu Val Ala Leu	Phe Thr Asp His Gln	Trp
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Val Ala Pro Ala	Val Ala Ala Asp Leu	His Ala Gln Tyr Gly	Ser
	455	460	465
Pro Thr Tyr Phe	Tyr Ala Phe Tyr His	His Cys Gln Ser Glu	Met
	470	475	480
Lys Pro Ser Trp	Ala Asp Ser Ala His	Gly Asp Glu Val Pro	Tyr
	485	490	495
Val Phe Gly Ile	Pro Met Ile Gly Pro	Thr Glu Leu Phe Ser	Cys
	500	505	510
Asn Phe Ser Lys	Asn Asp Val Met Leu	Ser Ala Val Val Met	Thr
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Pro Gln Asp Thr	Lys Phe Ile His Thr	Lys Pro Asn Arg Phe	Glu
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Glu Val Ala Trp	Ser Lys Tyr Asn Pro	Lys Asp Gln Leu Tyr	Leu
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His Ile Gly Leu	Lys Pro Arg Val Arg	Asp His Tyr Arg Ala	Thr
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Lys Val Ala Phe	Trp Leu Glu Leu Val	Pro His Leu His Asn	Leu
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Pro Asp Met Thr	Ser Phe Pro Tyr Gly	Thr Arg Arg Ser Pro	Ala
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Lys Ile Trp Pro	Thr Thr Lys Arg Pro	Ala Ile Thr Pro Ala	Asn
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Asn Pro Lys His	Ser Lys Asp Pro His	Lys Thr Gly Pro Glu	Asp
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Thr Thr Val Leu	Ile Glu Thr Lys Arg	Asp Tyr Ser Thr Glu	Leu
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Ser Val Thr Ile	Ala Val Gly Ala Ser	Leu Leu Phe Leu Asn	Ile
	680	685	690
Leu Ala Phe Ala	Ala Leu Tyr Tyr Lys	Lys Asp Lys Arg Arg	His
	695	700	705
Glu Thr His Arg	Arg Pro Ser Pro Gln	Arg Asn Thr Thr Asn	Asp
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Thr	Leu	Arg	Leu	Thr	Cys	Pro	Pro	Asp	Tyr	Thr	Leu	Thr	Leu	Arg
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Arg	Ser	Pro	Asp	Asp	Ile	Pro	Leu	Met	Thr	Pro	Asn	Thr	Ile	Thr
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<210> 377

<211> 25

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 377

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<210> 378

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 378

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<210> 379

<211> 2461

<212> DNA

<213> Homo sapiens

<400> 379

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<211> 348

<212> PRT

<213> Homo sapiens

<400> 380

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				20				25						30

Leu	Leu	Leu	Gly	Ser	Gly	Gln	Gly	Pro	Gln	Gln	Val	Gly	Ala	Gly		35	40	45
Gln	Thr	Phe	Glu	Tyr	Leu	Lys	Arg	Glu	His	Ser	Leu	Ser	Lys	Pro		50	55	60
Tyr	Gln	Gly	Val	Gly	Thr	Gly	Ser	Ser	Ser	Leu	Trp	Asn	Leu	Met		65	70	75
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Met	Gln	Ser	Lys	Gln	Gly	Ala	Leu	Trp	Asn	Arg	Val	Pro	Cys	Phe		95	100	105
Leu	Arg	Asp	Trp	Glu	Leu	Gln	Val	His	Phe	Lys	Ile	His	Gly	Gln		110	115	120
Gly	Lys	Lys	Asn	Leu	His	Gly	Asp	Gly	Leu	Ala	Ile	Trp	Tyr	Thr		125	130	135
Lys	Asp	Arg	Met	Gln	Pro	Gly	Pro	Val	Phe	Gly	Asn	Met	Asp	Lys		140	145	150
Phe	Val	Gly	Leu	Gly	Val	Phe	Val	Asp	Thr	Tyr	Pro	Asn	Glu	Glu		155	160	165
Lys	Gln	Gln	Glu	Arg	Val	Phe	Pro	Tyr	Ile	Ser	Ala	Met	Val	Asn		170	175	180
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Thr	Phe	Leu	Val	Ile	Arg	Tyr	Val	Lys	Arg	His	Leu	Thr	Ile	Met		215	220	225
Met	Asp	Ile	Asp	Gly	Lys	His	Glu	Trp	Arg	Asp	Cys	Ile	Glu	Val		230	235	240
Pro	Gly	Val	Arg	Leu	Pro	Arg	Gly	Tyr	Tyr	Phe	Gly	Thr	Ser	Ser		245	250	255
Ile	Thr	Gly	Asp	Leu	Ser	Asp	Asn	His	Asp	Val	Ile	Ser	Leu	Lys		260	265	270
Leu	Phe	Glu	Leu	Thr	Val	Glu	Arg	Thr	Pro	Glu	Glu	Glu	Lys	Leu		275	280	285
His	Arg	Asp	Val	Phe	Leu	Pro	Ser	Val	Asp	Asn	Met	Lys	Leu	Pro		290	295	300
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<223> Synthetic oligonucleotide probe

<400> 381

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<210> 382

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 382

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<212> DNA

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<400> 383

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<210> 384

<211> 3150

<212> DNA

<213> Homo sapiens

<400> 384

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<210> 385

<211> 480

<212> PRT

<213> Homo sapiens

<400> 385

Met	Leu	Phe	Arg	Asn	Arg	Phe	Leu	Leu	Leu	Leu	Ala	Leu	Ala	Ala
1				5					10					15

Leu	Leu	Ala	Phe	Val	Ser	Leu	Ser	Leu	Gln	Phe	Phe	His	Leu	Ile
				20					25					30

Pro	Val	Ser	Thr	Pro	Lys	Asn	Gly	Met	Ser	Ser	Lys	Ser	Arg	Lys
				35					40					45

Arg	Ile	Met	Pro	Asp	Pro	Val	Thr	Glu	Pro	Pro	Val	Thr	Asp	Pro
				50					55					60

Val	Tyr	Glu	Ala	Leu	Leu	Tyr	Cys	Asn	Ile	Pro	Ser	Val	Ala	Glu
				65					70					75

Arg	Ser	Met	Glu	Gly	His	Ala	Pro	His	His	Phe	Lys	Leu	Val	Ser
				80					85					90

Val	His	Val	Phe	Ile	Arg	His	Gly	Asp	Arg	Tyr	Pro	Leu	Tyr	Val
				95					100					105

Ile	Pro	Lys	Thr	Lys	Arg	Pro	Glu	Ile	Asp	Cys	Thr	Leu	Val	Ala
				110					115					120

Asn	Arg	Lys	Pro	Tyr	His	Pro	Lys	Leu	Glu	Ala	Phe	Ile	Ser	His
				125					130					135

Met	Ser	Lys	Gly	Ser	Gly	Ala	Ser	Phe	Glu	Ser	Pro	Leu	Asn	Ser
				140					145					150

Leu	Pro	Leu	Tyr	Pro	Asn	His	Pro	Leu	Cys	Glu	Met	Gly	Glu	Leu
				155					160					165

Thr	Gln	Thr	Gly	Val	Val	Gln	His	Leu	Gln	Asn	Gly	Gln	Leu	Leu
				170					175					180

Arg	Asp	Ile	Tyr	Leu	Lys	Lys	His	Lys	Leu	Leu	Pro	Asn	Asp	Trp
				185					190					195

Ser	Ala	Asp	Gln	Leu	Tyr	Leu	Glu	Thr	Thr	Gly	Lys	Ser	Arg	Thr
				200					205					210

Leu	Gln	Ser	Gly	Leu	Ala	Leu	Leu	Tyr	Gly	Phe	Leu	Pro	Asp	Phe
				215					220					225

Asp	Trp	Lys	Lys	Ile	Tyr	Phe	Arg	His	Gln	Pro	Ser	Ala	Leu	Phe
				230					235					240

Cys	Ser	Gly	Ser	Cys	Tyr	Cys	Pro	Val	Arg	Asn	Gln	Tyr	Leu	Glu
				245					250					255
Lys	Glu	Gln	Arg	Arg	Gln	Tyr	Leu	Leu	Arg	Leu	Lys	Asn	Ser	Gln
				260					265					270
Leu	Glu	Lys	Thr	Tyr	Gly	Glu	Met	Ala	Lys	Ile	Val	Asp	Val	Pro
				275					280					285
Thr	Lys	Gln	Leu	Arg	Ala	Ala	Asn	Pro	Ile	Asp	Ser	Met	Leu	Cys
				290					295					300
His	Phe	Cys	His	Asn	Val	Ser	Phe	Pro	Cys	Thr	Arg	Asn	Gly	Cys
				305					310					315
Val	Asp	Met	Glu	His	Phe	Lys	Val	Ile	Lys	Thr	His	Gln	Ile	Glu
				320					325					330
Asp	Glu	Arg	Glu	Arg	Arg	Glu	Lys	Lys	Leu	Tyr	Phe	Gly	Tyr	Ser
				335					340					345
Leu	Leu	Gly	Ala	His	Pro	Ile	Leu	Asn	Gln	Thr	Ile	Gly	Arg	Met
				350					355					360
Gln	Arg	Ala	Thr	Glu	Gly	Arg	Lys	Glu	Glu	Leu	Phe	Ala	Leu	Tyr
				365					370					375
Ser	Ala	His	Asp	Val	Thr	Leu	Ser	Pro	Val	Leu	Ser	Ala	Leu	Gly
				380					385					390
Leu	Ser	Glu	Ala	Arg	Phe	Pro	Arg	Phe	Ala	Ala	Arg	Leu	Ile	Phe
				395					400					405
Glu	Leu	Trp	Gln	Asp	Arg	Glu	Lys	Pro	Ser	Glu	His	Ser	Val	Arg
				410					415					420
Ile	Leu	Tyr	Asn	Gly	Val	Asp	Val	Thr	Phe	His	Thr	Ser	Phe	Cys
				425					430					435
Gln	Asp	His	His	Lys	Arg	Ser	Pro	Lys	Pro	Met	Cys	Pro	Leu	Glu
				440					445					450
Asn	Leu	Val	Arg	Phe	Val	Lys	Arg	Asp	Met	Phe	Val	Ala	Leu	Gly
				455					460					465
Gly	Ser	Gly	Thr	Asn	Tyr	Tyr	Asp	Ala	Cys	His	Arg	Glu	Gly	Phe
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<210> 386

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<210> 387  
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<400> 387  
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<210> 388  
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<220>  
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<210> 389  
<211> 3313  
<212> DNA  
<213> Homo sapiens

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atcctttctg ggagttcaag attgtgcagt aattgggttag gactctgagc 150  
gccgctgttc accaatcggg gagagaaaag cggagatcct gctcgccttg 200  
cacgcgcctg aagcaciaag cagatagcta ggaatgaacc atccctggga 250  
gtatgtggaa acaacggagg agctctgact tcccaactgt cccattctat 300  
gggcgaagga actgctcctg acttcagtgg ttaagggcag aattgaaaat 350  
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<210> 390

<211> 916

<212> PRT

<213> Homo sapiens

<400> 390

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Ile	Arg	Tyr	Ser	Val	Pro	Glu	Glu	Leu	Glu	Lys	Gly	Ser	Arg	Val		35	40	45	
Gly	Asp	Ile	Ser	Arg	Asp	Leu	Gly	Leu	Glu	Pro	Arg	Glu	Leu	Ala		50	55	60	
Glu	Arg	Gly	Val	Arg	Ile	Ile	Pro	Arg	Gly	Arg	Thr	Gln	Leu	Phe		65	70	75	
Ala	Leu	Asn	Pro	Arg	Ser	Gly	Ser	Leu	Val	Thr	Ala	Gly	Arg	Ile		80	85	90	
Asp	Arg	Glu	Glu	Leu	Cys	Met	Gly	Ala	Ile	Lys	Cys	Gln	Leu	Asn		95	100	105	
Leu	Asp	Ile	Leu	Met	Glu	Asp	Lys	Val	Lys	Ile	Tyr	Gly	Val	Glu		110	115	120	
Val	Glu	Val	Arg	Asp	Ile	Asn	Asp	Asn	Ala	Pro	Tyr	Phe	Arg	Glu		125	130	135	
Ser	Glu	Leu	Glu	Ile	Lys	Ile	Ser	Glu	Asn	Ala	Ala	Thr	Glu	Met		140	145	150	
Arg	Phe	Pro	Leu	Pro	His	Ala	Trp	Asp	Pro	Asp	Ile	Gly	Lys	Asn		155	160	165	
Ser	Leu	Gln	Ser	Tyr	Glu	Leu	Ser	Pro	Asn	Thr	His	Phe	Ser	Leu		170	175	180	
Ile	Val	Gln	Asn	Gly	Ala	Asp	Gly	Ser	Lys	Tyr	Pro	Glu	Leu	Val		185	190	195	
Leu	Lys	Arg	Ala	Leu	Asp	Arg	Glu	Glu	Lys	Ala	Ala	His	His	Leu		200	205	210	
Val	Leu	Thr	Ala	Ser	Asp	Gly	Gly	Asp	Pro	Val	Arg	Thr	Gly	Thr		215	220	225	
Ala	Arg	Ile	Arg	Val	Met	Val	Leu	Asp	Ala	Asn	Asp	Asn	Ala	Pro		230	235	240	
Ala	Phe	Ala	Gln	Pro	Glu	Tyr	Arg	Ala	Ser	Val	Pro	Glu	Asn	Leu		245	250	255	
Ala	Leu	Gly	Thr	Gln	Leu	Leu	Val	Val	Asn	Ala	Thr	Asp	Pro	Asp		260	265	270	
Glu	Gly	Val	Asn	Ala	Glu	Val	Arg	Tyr	Ser	Phe	Arg	Tyr	Val	Asp		275	280	285	

Asp	Lys	Ala	Ala	Gln	Val	Phe	Lys	Leu	Asp	Cys	Asn	Ser	Gly	Thr	
				290					295					300	
Ile	Ser	Thr	Ile	Gly	Glu	Leu	Asp	His	Glu	Glu	Ser	Gly	Phe	Tyr	
				305					310					315	
Gln	Met	Glu	Val	Gln	Ala	Met	Asp	Asn	Ala	Gly	Tyr	Ser	Ala	Arg	
				320					325					330	
Ala	Lys	Val	Leu	Ile	Thr	Val	Leu	Asp	Val	Asn	Asp	Asn	Ala	Pro	
				335					340					345	
Glu	Val	Val	Leu	Thr	Ser	Leu	Ala	Ser	Ser	Val	Pro	Glu	Asn	Ser	
				350					355					360	
Pro	Arg	Gly	Thr	Leu	Ile	Ala	Leu	Leu	Asn	Val	Asn	Asp	Gln	Asp	
				365					370					375	
Ser	Glu	Glu	Asn	Gly	Gln	Val	Ile	Cys	Phe	Ile	Gln	Gly	Asn	Leu	
				380					385					390	
Pro	Phe	Lys	Leu	Glu	Lys	Ser	Tyr	Gly	Asn	Tyr	Tyr	Ser	Leu	Val	
				395					400					405	
Thr	Asp	Ile	Val	Leu	Asp	Arg	Glu	Gln	Val	Pro	Ser	Tyr	Asn	Ile	
				410					415					420	
Thr	Val	Thr	Ala	Thr	Asp	Arg	Gly	Thr	Pro	Pro	Leu	Ser	Thr	Glu	
				425					430					435	
Thr	His	Ile	Ser	Leu	Asn	Val	Ala	Asp	Thr	Asn	Asp	Asn	Pro	Pro	
				440					445					450	
Val	Phe	Pro	Gln	Ala	Ser	Tyr	Ser	Ala	Tyr	Ile	Pro	Glu	Asn	Asn	
				455					460					465	
Pro	Arg	Gly	Val	Ser	Leu	Val	Ser	Val	Thr	Ala	His	Asp	Pro	Asp	
				470					475					480	
Cys	Glu	Glu	Asn	Ala	Gln	Ile	Thr	Tyr	Ser	Leu	Ala	Glu	Asn	Thr	
				485					490					495	
Ile	Gln	Gly	Ala	Ser	Leu	Ser	Ser	Tyr	Val	Ser	Ile	Asn	Ser	Asp	
				500					505					510	
Thr	Gly	Val	Leu	Tyr	Ala	Leu	Ser	Ser	Phe	Asp	Tyr	Glu	Gln	Phe	
				515					520					525	
Arg	Asp	Leu	Gln	Val	Lys	Val	Met	Ala	Arg	Asp	Asn	Gly	His	Pro	
				530					535					540	
Pro	Leu	Ser	Ser	Asn	Val	Ser	Leu	Ser	Leu	Phe	Val	Leu	Asp	Gln	
				545					550					555	
Asn	Asp	Asn	Ala	Pro	Glu	Ile	Leu	Tyr	Pro	Ala	Leu	Pro	Thr	Asp	
				560					565					570	



Gly Ser Thr Gly	Val Glu Leu Ala Pro	Arg Ser Ala Glu Pro Gly	575	580	585
Tyr Leu Val Thr	Lys Val Val Ala Val	Asp Arg Asp Ser Gly Gln	590	595	600
Asn Ala Trp Leu	Ser Tyr Arg Leu Leu	Lys Ala Ser Glu Pro Gly	605	610	615
Leu Phe Ser Val	Gly Leu His Thr Gly	Glu Val Arg Thr Ala Arg	620	625	630
Ala Leu Leu Asp	Arg Asp Ala Leu Lys	Gln Ser Leu Val Val Ala	635	640	645
Val Gln Asp His	Gly Gln Pro Pro Leu	Ser Ala Thr Val Thr Leu	650	655	660
Thr Val Ala Val	Ala Asp Ser Ile Pro	Gln Val Leu Ala Asp Leu	665	670	675
Gly Ser Leu Glu	Ser Pro Ala Asn Ser	Glu Thr Ser Asp Leu Thr	680	685	690
Leu Tyr Leu Val	Val Ala Val Ala Ala	Val Ser Cys Val Phe Leu	695	700	705
Ala Phe Val Ile	Leu Leu Leu Ala Leu	Arg Leu Arg Arg Trp His	710	715	720
Lys Ser Arg Leu	Leu Gln Ala Ser Gly	Gly Gly Leu Thr Gly Ala	725	730	735
Pro Ala Ser His	Phe Val Gly Val Asp	Gly Val Gln Ala Phe Leu	740	745	750
Gln Thr Tyr Ser	His Glu Val Ser Leu	Thr Thr Asp Ser Arg Lys	755	760	765
Ser His Leu Ile	Phe Pro Gln Pro Asn	Tyr Ala Asp Met Leu Val	770	775	780
Ser Gln Glu Ser	Phe Glu Lys Ser Glu	Pro Leu Leu Leu Ser Gly	785	790	795
Asp Ser Val Phe	Ser Lys Asp Ser His	Gly Leu Ile Glu Val Ser	800	805	810
Leu Tyr Gln Ile	Phe Phe Leu Phe Phe	Phe Asn Cys Ser Val Ser	815	820	825
Gln Ala Gly Val	Gln Arg Tyr Asp His	Ser Ser Leu Arg Pro Gln	830	835	840
Thr Pro Arg Leu	Lys Gln Leu Ser His	Leu Cys Leu Arg Cys Asn	845	850	855

Arg	Asp	Tyr	Arg	Cys	Lys	Pro	Pro	Thr	Val	Cys	Leu	Ser	Ile	Tyr
				860					865					870
Leu	Ser	Ile	Tyr	Leu	Ser	Ile	Tyr	Leu	Ser	Ile	Tyr	Leu	Leu	Leu
				875					880					885
Ser	Cys	Thr	Asp	Gly	Ser	Leu	Thr	Pro	Val	Ile	Pro	Val	Leu	Trp
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Glu	Ala	Glu	Ala	Gly	Gly	Ser	Pro	Glu	Val	Gly	Ser	Leu	Arg	Pro
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<210> 391  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 391  
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<210> 392  
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<400> 392  
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<210> 393  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
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<400> 393  
 ccgactgtga aagagaacgc cccagatcca cttgttcccc 40

<210> 394  
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 <212> DNA  
 <213> Homo sapiens

<400> 394  
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cccagttaaa aggctccaga atcgtgtacc aggagagaa ctgaagtact 100

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<210> 395

<211> 260

<212> PRT

<213> Homo sapiens

<400> 395

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			20						25					30
Asp	Lys	Val	Leu	Gly	Gly	His	Glu	Cys	Gln	Pro	His	Ser	Gln	Pro
			35						40					45
Trp	Gln	Ala	Ala	Leu	Phe	Gln	Gly	Gln	Gln	Leu	Leu	Cys	Gly	Gly
			50						55					60
Val	Leu	Val	Gly	Gly	Asn	Trp	Val	Leu	Thr	Ala	Ala	His	Cys	Lys
			65						70					75

Lys	Pro	Lys	Tyr	Thr	Val	Arg	Leu	Gly	Asp	His	Ser	Leu	Gln	Asn	80	85	90
Lys	Asp	Gly	Pro	Glu	Gln	Glu	Ile	Pro	Val	Val	Gln	Ser	Ile	Pro	95	100	105
His	Pro	Cys	Tyr	Asn	Ser	Ser	Asp	Val	Glu	Asp	His	Asn	His	Asp	110	115	120
Leu	Met	Leu	Leu	Gln	Leu	Arg	Asp	Gln	Ala	Ser	Leu	Gly	Ser	Lys	125	130	135
Val	Lys	Pro	Ile	Ser	Leu	Ala	Asp	His	Cys	Thr	Gln	Pro	Gly	Gln	140	145	150
Lys	Cys	Thr	Val	Ser	Gly	Trp	Gly	Thr	Val	Thr	Ser	Pro	Arg	Glu	155	160	165
Asn	Phe	Pro	Asp	Thr	Leu	Asn	Cys	Ala	Glu	Val	Lys	Ile	Phe	Pro	170	175	180
Gln	Lys	Lys	Cys	Glu	Asp	Ala	Tyr	Pro	Gly	Gln	Ile	Thr	Asp	Gly	185	190	195
Met	Val	Cys	Ala	Gly	Ser	Ser	Lys	Gly	Ala	Asp	Thr	Cys	Gln	Gly	200	205	210
Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asp	Gly	Ala	Leu	Gln	Gly	Ile	215	220	225
Thr	Ser	Trp	Gly	Ser	Asp	Pro	Cys	Gly	Arg	Ser	Asp	Lys	Pro	Gly	230	235	240
Val	Tyr	Thr	Asn	Ile	Cys	Arg	Tyr	Leu	Asp	Trp	Ile	Lys	Lys	Ile	245	250	255
Ile	Gly	Ser	Lys	Gly											260		

<210> 396

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 396

cagcctacag aataaagatg gcc 24

<210> 397

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 397

ggtgcaatga tctgccaggc tgat 24

<210> 398

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 398

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<210> 399

<211> 2236

<212> DNA

<213> Homo sapiens

<400> 399

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gccccgcgcc gggccgcgc ccgcgcgcgc gccaggtga gcgctccgcc 150

cgccgcgagg ccccgcccc gcccgccccc gccccgcgcc ggccggcggg 200

ggaaccgggc ggattcctcg cgcgtcaaac cacctgatcc cataaaacat 250

tcatectccc ggcgggccgc gctgcgagcg ccccgccagt ccgcgcgcgc 300

gccgccctcg ccctgtgcgc cctgcgcgcc ctgcgcaccc gcggcccgag 350

cccagccaga gccgggcgga gcggagcgcg ccgagcctcg tcccgcggcc 400

gggcccgggc cgggcccgtag cggcggcgcc tggatgcgga cccggccgcg 450

gggagacggg cgcccgcgcc gaaacgactt tcagtccccg acgcgccccg 500

cccaaccctt acgatgaaga gggcgctccgc tggaggagc cggctgctgg 550

catgggtgct gtggctgcag gcctggcagg tggcagcccc atgcccaggt 600

gcctgcgtat gctacaatga gcccaaggty acgacaagct gccccagca 650

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tctgcacgg caaccgcatc tcgcatgtgc cagctgccag cttccgtgcc 750

tgccgcaacc tcaccatcct gtggctgcac tcgaatgtgc tggcccgaat 800

tgatgcggct gccttcaact gcctggccct cctggagcag ctggacctca 850

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<210> 400

<211> 473

<212> PRT  
<213> Homo sapiens

<400> 400

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				20					25					30	
Cys	Val	Cys	Tyr	Asn	Glu	Pro	Lys	Val	Thr	Thr	Ser	Cys	Pro	Gln	
				35					40					45	
Gln	Gly	Leu	Gln	Ala	Val	Pro	Val	Gly	Ile	Pro	Ala	Ala	Ser	Gln	
				50					55					60	
Arg	Ile	Phe	Leu	His	Gly	Asn	Arg	Ile	Ser	His	Val	Pro	Ala	Ala	
				65					70					75	
Ser	Phe	Arg	Ala	Cys	Arg	Asn	Leu	Thr	Ile	Leu	Trp	Leu	His	Ser	
				80					85					90	
Asn	Val	Leu	Ala	Arg	Ile	Asp	Ala	Ala	Ala	Phe	Thr	Gly	Leu	Ala	
				95					100					105	
Leu	Leu	Glu	Gln	Leu	Asp	Leu	Ser	Asp	Asn	Ala	Gln	Leu	Arg	Ser	
				110					115					120	
Val	Asp	Pro	Ala	Thr	Phe	His	Gly	Leu	Gly	Arg	Leu	His	Thr	Leu	
				125					130					135	
His	Leu	Asp	Arg	Cys	Gly	Leu	Gln	Glu	Leu	Gly	Pro	Gly	Leu	Phe	
				140					145					150	
Arg	Gly	Leu	Ala	Ala	Leu	Gln	Tyr	Leu	Tyr	Leu	Gln	Asp	Asn	Ala	
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				170					175					180	
Thr	His	Leu	Phe	Leu	His	Gly	Asn	Arg	Ile	Ser	Ser	Val	Pro	Glu	
				185					190					195	
Arg	Ala	Phe	Arg	Gly	Leu	His	Ser	Leu	Asp	Arg	Leu	Leu	Leu	His	
				200					205					210	
Gln	Asn	Arg	Val	Ala	His	Val	His	Pro	His	Ala	Phe	Arg	Asp	Leu	
				215					220					225	
Gly	Arg	Leu	Met	Thr	Leu	Tyr	Leu	Phe	Ala	Asn	Asn	Leu	Ser	Ala	
				230					235					240	
Leu	Pro	Thr	Glu	Ala	Leu	Ala	Pro	Leu	Arg	Ala	Leu	Gln	Tyr	Leu	
				245					250					255	
Arg	Leu	Asn	Asp	Asn	Pro	Trp	Val	Cys	Asp	Cys	Arg	Ala	Arg	Pro	
				260					265					270	

Leu Trp Ala Trp	Leu Gln Lys Phe Arg	Gly Ser Ser Ser Glu Val	
275	280	285	
Pro Cys Ser Leu	Pro Gln Arg Leu Ala	Gly Arg Asp Leu Lys Arg	
290	295	300	
Leu Ala Ala Asn	Asp Leu Gln Gly Cys	Ala Val Ala Thr Gly Pro	
305	310	315	
Tyr His Pro Ile	Trp Thr Gly Arg Ala	Thr Asp Glu Glu Pro Leu	
320	325	330	
Gly Leu Pro Lys	Cys Cys Gln Pro Asp	Ala Ala Asp Lys Ala Ser	
335	340	345	
Val Leu Glu Pro	Gly Arg Pro Ala Ser	Ala Gly Asn Ala Leu Lys	
350	355	360	
Gly Arg Val Pro	Pro Gly Asp Ser Pro	Pro Gly Asn Gly Ser Gly	
365	370	375	
Pro Arg His Ile	Asn Asp Ser Pro Phe	Gly Thr Leu Pro Gly Ser	
380	385	390	
Ala Glu Pro Pro	Leu Thr Ala Val Arg	Pro Glu Gly Ser Glu Pro	
395	400	405	
Pro Gly Phe Pro	Thr Ser Gly Pro Arg	Arg Arg Pro Gly Cys Ser	
410	415	420	
Arg Lys Asn Arg	Thr Arg Ser His Cys	Arg Leu Gly Gln Ala Gly	
425	430	435	
Ser Gly Gly Gly	Gly Thr Gly Asp Ser	Glu Gly Ser Gly Ala Leu	
440	445	450	
Pro Ser Leu Thr	Cys Ser Leu Thr Pro	Leu Gly Leu Ala Leu Val	
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Leu Trp Thr Val	Leu Gly Pro Cys		
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<211> 24

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<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 401

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<210> 402

<211> 24

<212> DNA



<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 402

ccctgcaggt cattggcagc tagg 24

<210> 403

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 403

aggcactgcc tgatgacacc ttccgcgacc tgggcaacct cacac 45

<210> 404

<211> 2738

<212> DNA

<213> Homo sapiens

<400> 404

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agctgaatcc agcaagaaca atggaggcca gcgggaagct catttgca 200

caaaggcaag tccttttttc ctttctcctt ttgggcttat ctctggcggg 250

cgcggcggaa cctagaagct attctgtggt ggaggaaact gagggcagct 300

cctttgtcac caatttagca aaggacctgg gtctggagca gagggaattc 350

tccaggcggg gggtaggggt tgtttccaga gggaacaaac tacatttgca 400

gctcaatcag gagaccgcgg atttgttgct aaatgagaaa ttggaccgtg 450

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<210> 405  
 <211> 798  
 <212> PRT  
 <213> Homo sapiens

<400> 405  
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 Pro Arg Ser Tyr Ser Val Val Glu Glu Thr Glu Gly Ser Ser Phe  
 35 40 45  
 Val Thr Asn Leu Ala Lys Asp Leu Gly Leu Glu Gln Arg Glu Phe  
 50 55 60  
 Ser Arg Arg Gly Val Arg Val Val Ser Arg Gly Asn Lys Leu His  
 65 70 75  
 Leu Gln Leu Asn Gln Glu Thr Ala Asp Leu Leu Leu Asn Glu Lys  
 80 85 90  
 Leu Asp Arg Glu Asp Leu Cys Gly His Thr Glu Pro Cys Val Leu  
 95 100 105  
 Arg Phe Gln Val Leu Leu Glu Ser Pro Phe Glu Phe Phe Gln Ala  
 110 115 120  
 Glu Leu Gln Val Ile Asp Ile Asn Asp His Ser Pro Val Phe Leu  
 125 130 135  
 Asp Lys Gln Met Leu Val Lys Val Ser Glu Ser Ser Pro Pro Gly  
 140 145 150

Thr	Thr	Phe	Pro	Leu	Lys	Asn	Ala	Glu	Asp	Leu	Asp	Val	Gly	Gln	155	160	165
Asn	Asn	Ile	Glu	Asn	Tyr	Ile	Ile	Ser	Pro	Asn	Ser	Tyr	Phe	Arg	170	175	180
Val	Leu	Thr	Arg	Lys	Arg	Ser	Asp	Gly	Arg	Lys	Tyr	Pro	Glu	Leu	185	190	195
Val	Leu	Asp	Lys	Ala	Leu	Asp	Arg	Glu	Glu	Glu	Ala	Glu	Leu	Arg	200	205	210
Leu	Thr	Leu	Thr	Ala	Leu	Asp	Gly	Gly	Ser	Pro	Pro	Arg	Ser	Gly	215	220	225
Thr	Ala	Gln	Val	Tyr	Ile	Glu	Val	Leu	Asp	Val	Asn	Asp	Asn	Ala	230	235	240
Pro	Glu	Phe	Glu	Gln	Pro	Phe	Tyr	Arg	Val	Gln	Ile	Ser	Glu	Asp	245	250	255
Ser	Pro	Val	Gly	Phe	Leu	Val	Val	Lys	Val	Ser	Ala	Thr	Asp	Val	260	265	270
Asp	Thr	Gly	Val	Asn	Gly	Glu	Ile	Ser	Tyr	Ser	Leu	Phe	Gln	Ala	275	280	285
Ser	Glu	Glu	Ile	Gly	Lys	Thr	Phe	Lys	Ile	Asn	Pro	Leu	Thr	Gly	290	295	300
Glu	Ile	Glu	Leu	Lys	Lys	Gln	Leu	Asp	Phe	Glu	Lys	Leu	Gln	Ser	305	310	315
Tyr	Glu	Val	Asn	Ile	Glu	Ala	Arg	Asp	Ala	Gly	Thr	Phe	Ser	Gly	320	325	330
Lys	Cys	Thr	Val	Leu	Ile	Gln	Val	Ile	Asp	Val	Asn	Asp	His	Ala	335	340	345
Pro	Glu	Val	Thr	Met	Ser	Ala	Phe	Thr	Ser	Pro	Ile	Pro	Glu	Asn	350	355	360
Ala	Pro	Glu	Thr	Val	Val	Ala	Leu	Phe	Ser	Val	Ser	Asp	Leu	Asp	365	370	375
Ser	Gly	Glu	Asn	Gly	Lys	Ile	Ser	Cys	Ser	Ile	Gln	Glu	Asp	Leu	380	385	390
Pro	Phe	Leu	Leu	Lys	Ser	Ala	Glu	Asn	Phe	Tyr	Thr	Leu	Leu	Thr	395	400	405
Glu	Arg	Pro	Leu	Asp	Arg	Glu	Ser	Arg	Ala	Glu	Tyr	Asn	Ile	Thr	410	415	420
Ile	Thr	Val	Thr	Asp	Leu	Gly	Thr	Pro	Met	Leu	Ile	Thr	Gln	Leu	425	430	435

Asn Met Thr Val	Leu Ile Ala Asp Val	Asn Asp Asn Ala Pro	Ala
	440	445	450
Phe Thr Gln Thr	Ser Tyr Thr Leu Phe	Val Arg Glu Asn Asn	Ser
	455	460	465
Pro Ala Leu His	Ile Arg Ser Val Ser	Ala Thr Asp Arg Asp	Ser
	470	475	480
Gly Thr Asn Ala	Gln Val Thr Tyr Ser	Leu Leu Pro Pro Gln	Asp
	485	490	495
Pro His Leu Pro	Leu Thr Ser Leu Val	Ser Ile Asn Ala Asp	Asn
	500	505	510
Gly His Leu Phe	Ala Leu Arg Ser Leu	Asp Tyr Glu Ala Leu	Gln
	515	520	525
Gly Phe Gln Phe	Arg Val Gly Ala Ser	Asp His Gly Ser Pro	Ala
	530	535	540
Leu Ser Ser Glu	Ala Leu Val Arg Val	Val Val Leu Asp Ala	Asn
	545	550	555
Asp Asn Ser Pro	Phe Val Leu Tyr Pro	Leu Gln Asn Gly Ser	Ala
	560	565	570
Pro Cys Thr Glu	Leu Val Pro Arg Ala	Ala Glu Pro Gly Tyr	Leu
	575	580	585
Val Thr Lys Val	Val Ala Val Asp Gly	Asp Ser Gly Gln Asn	Ala
	590	595	600
Trp Leu Ser Tyr	Gln Leu Leu Lys Ala	Thr Glu Leu Gly Leu	Phe
	605	610	615
Gly Val Trp Ala	His Asn Gly Glu Val	Arg Thr Ala Arg Leu	Leu
	620	625	630
Ser Glu Arg Asp	Ala Ala Lys His Arg	Leu Val Val Leu Val	Lys
	635	640	645
Asp Asn Gly Glu	Pro Pro Arg Ser Ala	Thr Ala Thr Leu His	Val
	650	655	660
Leu Leu Val Asp	Gly Phe Ser Gln Pro	Tyr Leu Pro Leu Pro	Glu
	665	670	675
Ala Ala Pro Thr	Gln Ala Gln Ala Asp	Leu Leu Thr Val Tyr	Leu
	680	685	690
Val Val Ala Leu	Ala Ser Val Ser Ser	Leu Phe Leu Phe Ser	Val
	695	700	705
Leu Leu Phe Val	Ala Val Arg Leu Cys	Arg Arg Ser Arg Ala	Ala
	710	715	720

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Leu	Val	Asp	Met	Ser	Gly	Thr	Arg	Thr	Leu	Ser	Gln	Ser	Tyr	Gln
				740					745					750
Tyr	Glu	Val	Cys	Leu	Ala	Gly	Gly	Ser	Gly	Thr	Asn	Glu	Phe	Lys
				755					760					765
Phe	Leu	Lys	Pro	Ile	Ile	Pro	Asn	Phe	Pro	Pro	Gln	Cys	Pro	Gly
				770					775					780
Lys	Glu	Ile	Gln	Gly	Asn	Ser	Thr	Phe	Pro	Asn	Asn	Phe	Gly	Phe
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Asn Ile Gln

<210> 406

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 406

ctgagaacgc gcctgaaact gtg 23

<210> 407

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 407

agcgttgtca ttgacatcg cg 22

<210> 408

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 408

ttagttgtct cattcaggag gatctaccct tcctcctgaa atccgcggaa 50

<210> 409

<211> 1379

<212> DNA

<213> Homo sapiens

<400> 409

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 cggtcgacga ccgccccgcg tcatgcggct cctcggctgg tggcaagtat 150  
 tgctgtgggt gctgggactt cccgtccgcg gcgtggaggt tgcagaggaa 200  
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 gatcacatgg tgatgctgtc tgtgattcct ggggaagctg aggacaaagt 400  
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<211> 360  
<212> PRT  
<213> Homo sapiens

<400> 410

Met	Val	Pro	Ala	Ala	Gly	Arg	Arg	Pro	Pro	Arg	Val	Met	Arg	Leu
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Leu	Gly	Trp	Trp	Gln	Val	Leu	Leu	Trp	Val	Leu	Gly	Leu	Pro	Val
				20					25					30
Arg	Gly	Val	Glu	Val	Ala	Glu	Glu	Ser	Gly	Arg	Leu	Trp	Ser	Glu
				35					40					45
Glu	Gln	Pro	Ala	His	Pro	Leu	Gln	Val	Gly	Ala	Val	Tyr	Leu	Gly
				50					55					60
Glu	Glu	Glu	Leu	Leu	His	Asp	Pro	Met	Gly	Gln	Asp	Arg	Ala	Ala
				65					70					75
Glu	Glu	Ala	Asn	Ala	Val	Leu	Gly	Leu	Asp	Thr	Gln	Gly	Asp	His
				80					85					90
Met	Val	Met	Leu	Ser	Val	Ile	Pro	Gly	Glu	Ala	Glu	Asp	Lys	Val
				95					100					105
Ser	Ser	Glu	Pro	Ser	Gly	Val	Thr	Cys	Gly	Ala	Gly	Gly	Ala	Glu
				110					115					120
Asp	Ser	Arg	Cys	Asn	Val	Arg	Glu	Ser	Leu	Phe	Ser	Leu	Asp	Gly
				125					130					135
Ala	Gly	Ala	His	Phe	Pro	Asp	Arg	Glu	Glu	Glu	Tyr	Tyr	Thr	Glu
				140					145					150
Pro	Glu	Val	Ala	Glu	Ser	Asp	Ala	Ala	Pro	Thr	Glu	Asp	Ser	Asn
				155					160					165
Asn	Thr	Glu	Ser	Leu	Lys	Ser	Pro	Lys	Val	Asn	Cys	Glu	Glu	Arg
				170					175					180
Asn	Ile	Thr	Gly	Leu	Glu	Asn	Phe	Thr	Leu	Lys	Ile	Leu	Asn	Met
				185					190					195
Ser	Gln	Asp	Leu	Met	Asp	Phe	Leu	Asn	Pro	Asn	Gly	Ser	Asp	Cys
				200					205					210
Thr	Leu	Val	Leu	Phe	Tyr	Thr	Pro	Trp	Cys	Arg	Phe	Ser	Ala	Ser
				215					220					225
Leu	Ala	Pro	His	Phe	Asn	Ser	Leu	Pro	Arg	Ala	Phe	Pro	Ala	Leu
				230					235					240
His	Phe	Leu	Ala	Leu	Asp	Ala	Ser	Gln	His	Ser	Ser	Leu	Ser	Thr
				245					250					255
Arg	Phe	Gly	Thr	Val	Ala	Val	Pro	Asn	Ile	Leu	Leu	Phe	Gln	Gly



260	265	270
Ala Lys Pro Met	Ala Arg Phe Asn His Thr Asp Arg Thr Leu Glu	
275	280	285
Thr Leu Lys Ile	Phe Ile Phe Asn Gln Thr Gly Ile Glu Ala Lys	
290	295	300
Lys Asn Val Val	Val Thr Gln Ala Asp Gln Ile Gly Pro Leu Pro	
305	310	315
Ser Thr Leu Ile	Lys Ser Val Asp Trp Leu Leu Val Phe Ser Leu	
320	325	330
Phe Phe Leu Ile	Ser Phe Ile Met Tyr Ala Thr Ile Arg Thr Glu	
335	340	345
Ser Ile Arg Trp	Leu Ile Pro Gly Gln Glu Gln Glu His Val Glu	
350	355	360

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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 411

cacagagcca gaagtggcgg aatc 24

<210> 412

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 412

ccacatgttc ctgctcttgt cctgg 25

<210> 413

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 413

cggtagtgac tgtactctag tcctgtttta caccocgtgg tgccg 45

<210> 414

<211> 1196

<212> DNA

<213> Homo sapiens

<400> 414

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ggctcggcgc gcgggctctt cctctttggc cagcccgact tctcctacaa 150  
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<210> 415

<211> 295

<212> PRT

<213> Homo sapiens

<400> 415

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Pro Asp Phe Ser Tyr Lys Arg Ser Asn Cys Lys Pro Ile Pro Val	35	40	45
Asn Leu Gln Leu Cys His Gly Ile Glu Tyr Gln Asn Met Arg Leu	50	55	60
Pro Asn Leu Leu Gly His Glu Thr Met Lys Glu Val Leu Glu Gln	65	70	75
Ala Gly Ala Trp Ile Pro Leu Val Met Lys Gln Cys His Pro Asp	80	85	90
Thr Lys Lys Phe Leu Cys Ser Leu Phe Ala Pro Val Cys Leu Asp	95	100	105
Asp Leu Asp Glu Thr Ile Gln Pro Cys His Ser Leu Cys Val Gln	110	115	120
Val Lys Asp Arg Cys Ala Pro Val Met Ser Ala Phe Gly Phe Pro	125	130	135
Trp Pro Asp Met Leu Glu Cys Asp Arg Phe Pro Gln Asp Asn Asp	140	145	150
Leu Cys Ile Pro Leu Ala Ser Ser Asp His Leu Leu Pro Ala Thr	155	160	165
Glu Glu Ala Pro Lys Val Cys Glu Ala Cys Lys Asn Lys Asn Asp	170	175	180
Asp Asp Asn Asp Ile Met Glu Thr Leu Cys Lys Asn Asp Phe Ala	185	190	195
Leu Lys Ile Lys Val Lys Glu Ile Thr Tyr Ile Asn Arg Asp Thr	200	205	210
Lys Ile Ile Leu Glu Thr Lys Ser Lys Thr Ile Tyr Lys Leu Asn	215	220	225
Gly Val Ser Glu Arg Asp Leu Lys Lys Ser Val Leu Trp Leu Lys	230	235	240
Asp Ser Leu Gln Cys Thr Cys Glu Glu Met Asn Asp Ile Asn Ala	245	250	255
Pro Tyr Leu Val Met Gly Gln Lys Gln Gly Gly Glu Leu Val Ile	260	265	270
Thr Ser Val Lys Arg Trp Gln Lys Gly Gln Arg Glu Phe Lys Arg	275	280	285
Ile Ser Arg Ser Ile Arg Lys Leu Gln Cys			

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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 416  
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<210> 417  
 <211> 25  
 <212> DNA  
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<220>  
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<400> 417  
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<210> 418  
 <211> 47  
 <212> DNA  
 <213> Artificial Sequence

<220>  
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<400> 418  
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<210> 419  
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 <212> DNA  
 <213> Homo sapiens

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 cgctgggtgt tcctgctcgc gatcagcctg ctcaactgct ccaacgccac 150  
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 ccgtgcggcg accatcctgg gtgcgtggct gaactttgcc gggagtgtgc 350  
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<210> 420  
<211> 560  
<212> PRT  
<213> Homo sapiens

<400> 420

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				20					25					30	
Val	Phe	Leu	Leu	Ala	Ile	Ser	Leu	Leu	Asn	Cys	Ser	Asn	Ala	Thr	
				35					40					45	
Leu	Trp	Leu	Ser	Phe	Ala	Pro	Val	Ala	Asp	Val	Ile	Ala	Glu	Asp	
				50					55					60	
Leu	Val	Leu	Ser	Met	Glu	Gln	Ile	Asn	Trp	Leu	Ser	Leu	Val	Tyr	
				65					70					75	
Leu	Val	Val	Ser	Thr	Pro	Phe	Gly	Val	Ala	Ala	Ile	Trp	Ile	Leu	
				80					85					90	
Asp	Ser	Val	Gly	Leu	Arg	Ala	Ala	Thr	Ile	Leu	Gly	Ala	Trp	Leu	
				95					100					105	
Asn	Phe	Ala	Gly	Ser	Val	Leu	Arg	Met	Val	Pro	Cys	Met	Val	Val	
				110					115					120	
Gly	Thr	Gln	Asn	Pro	Phe	Ala	Phe	Leu	Met	Gly	Gly	Gln	Ser	Leu	
				125					130					135	
Cys	Ala	Leu	Ala	Gln	Ser	Leu	Val	Ile	Phe	Ser	Pro	Ala	Lys	Leu	
				140					145					150	
Ala	Ala	Leu	Trp	Phe	Pro	Glu	His	Gln	Arg	Ala	Thr	Ala	Asn	Met	
				155					160					165	
Leu	Ala	Thr	Met	Ser	Asn	Pro	Leu	Gly	Val	Leu	Val	Ala	Asn	Val	
				170					175					180	
Leu	Ser	Pro	Val	Leu	Val	Lys	Lys	Gly	Glu	Asp	Ile	Pro	Leu	Met	
				185					190					195	
Leu	Gly	Val	Tyr	Thr	Ile	Pro	Ala	Gly	Val	Val	Cys	Leu	Leu	Ser	
				200					205					210	
Thr	Ile	Cys	Leu	Trp	Glu	Ser	Val	Pro	Pro	Thr	Pro	Pro	Ser	Ala	
				215					220					225	
Gly	Ala	Ala	Ser	Ser	Thr	Ser	Glu	Lys	Phe	Leu	Asp	Gly	Leu	Lys	
				230					235					240	
Leu	Gln	Leu	Met	Trp	Asn	Lys	Ala	Tyr	Val	Ile	Leu	Ala	Val	Cys	
				245					250					255	

Leu Gly Gly Met	Ile Gly Ile Ser Ala	Ser Phe Ser Ala	Leu Leu
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Glu Gln Ile Leu Cys	Ala Ser Gly His	Ser Ser Gly Phe	Ser Gly
275	280	285	
Leu Cys Gly Ala	Leu Phe Ile Thr Phe	Gly Ile Leu Gly	Ala Leu
290	295	300	
Ala Leu Gly Pro	Tyr Val Asp Arg Thr	Lys His Phe Thr	Glu Ala
305	310	315	
Thr Lys Ile Gly	Leu Cys Leu Phe Ser	Leu Ala Cys Val	Pro Phe
320	325	330	
Ala Leu Val Ser	Gln Leu Gln Gly Gln	Thr Leu Ala Leu	Ala Ala
335	340	345	
Thr Cys Ser Leu	Leu Gly Leu Phe Gly	Phe Ser Val Gly	Pro Val
350	355	360	
Ala Met Glu Leu	Ala Val Glu Cys Ser	Phe Pro Val Gly	Glu Gly
365	370	375	
Ala Ala Thr Gly	Met Ile Phe Val Leu	Gly Gln Ala Glu	Gly Ile
380	385	390	
Leu Ile Met Leu	Ala Met Thr Ala Leu	Thr Val Arg Arg	Ser Glu
395	400	405	
Pro Ser Leu Ser	Thr Cys Gln Gln Gly	Glu Asp Pro Leu	Asp Trp
410	415	420	
Thr Val Ser Leu	Leu Leu Met Ala Gly	Leu Cys Thr Phe	Phe Ser
425	430	435	
Cys Ile Leu Ala	Val Phe Phe His Thr	Pro Tyr Arg Arg	Leu Gln
440	445	450	
Ala Glu Ser Gly	Glu Pro Pro Ser Thr	Arg Asn Ala Val	Gly Gly
455	460	465	
Ala Asp Ser Gly	Pro Gly Val Asp Arg	Gly Gly Ala Gly	Arg Ala
470	475	480	
Gly Val Leu Gly	Pro Ser Thr Ala Thr	Pro Glu Cys Thr	Ala Arg
485	490	495	
Gly Ala Ser Leu	Glu Asp Pro Arg Gly	Pro Gly Ser Pro	His Pro
500	505	510	
Ala Cys His Arg	Ala Thr Pro Arg Ala	Gln Gly Pro Ala	Ala Thr
515	520	525	
Asp Ala Pro Ser	Arg Pro Gly Arg Leu	Ala Gly Arg Val	Gln Ala
530	535	540	

Ser Arg Phe Ile Asp Pro Ala Gly Ser His Ser Ser Phe Ser Ser  
545 550 555

Pro Trp Val Ile Thr  
560

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<212> DNA  
<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 421  
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<210> 422  
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<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 422  
cggttcaata aacctggacg cttgg 25

<210> 423  
<211> 43  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 423  
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<210> 424  
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<212> DNA  
<213> Homo sapiens

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 agaggcagca gcagcagcag caggtgcctg tgaacatacc tcagacgcct 3900  
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 aaagggtcag tcctctggca gaacagatgc cacggagtat cacaggcagg 4200  
 aaagggtggc cttcttgggt agcaggagtc agggggctgt accctggggg 4250  
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<210> 425

<211> 1184

<212> PRT

<213> Homo sapiens

<400> 425

Met	Met	Gln	Leu	Leu	Gln	Leu	Leu	Leu	Gly	Leu	Leu	Gly	Pro	Gly
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Gly	Tyr	Leu	Phe	Leu	Leu	Gly	Asp	Cys	Gln	Glu	Val	Thr	Thr	Leu	20	25	30
Thr	Val	Lys	Tyr	Gln	Val	Ser	Glu	Glu	Val	Pro	Ser	Gly	Thr	Val	35	40	45
Ile	Gly	Lys	Leu	Ser	Gln	Glu	Leu	Gly	Arg	Glu	Glu	Arg	Arg	Arg	50	55	60
Gln	Ala	Gly	Ala	Ala	Phe	Gln	Val	Leu	Gln	Leu	Pro	Gln	Ala	Leu	65	70	75
Pro	Ile	Gln	Val	Asp	Ser	Glu	Glu	Gly	Leu	Leu	Ser	Thr	Gly	Arg	80	85	90
Arg	Leu	Asp	Arg	Glu	Gln	Leu	Cys	Arg	Gln	Trp	Asp	Pro	Cys	Leu	95	100	105
Val	Ser	Phe	Asp	Val	Leu	Ala	Thr	Gly	Asp	Leu	Ala	Leu	Ile	His	110	115	120
Val	Glu	Ile	Gln	Val	Leu	Asp	Ile	Asn	Asp	His	Gln	Pro	Arg	Phe	125	130	135
Pro	Lys	Gly	Glu	Gln	Glu	Leu	Glu	Ile	Ser	Glu	Ser	Ala	Ser	Leu	140	145	150
Arg	Thr	Arg	Ile	Pro	Leu	Asp	Arg	Ala	Leu	Asp	Pro	Asp	Thr	Gly	155	160	165
Pro	Asn	Thr	Leu	His	Thr	Tyr	Thr	Leu	Ser	Pro	Ser	Glu	His	Phe	170	175	180
Ala	Leu	Asp	Val	Ile	Val	Gly	Pro	Asp	Glu	Thr	Lys	His	Ala	Glu	185	190	195
Leu	Ile	Val	Val	Lys	Glu	Leu	Asp	Arg	Glu	Ile	His	Ser	Phe	Phe	200	205	210
Asp	Leu	Val	Leu	Thr	Ala	Tyr	Asp	Asn	Gly	Asn	Pro	Pro	Lys	Ser	215	220	225
Gly	Thr	Ser	Leu	Val	Lys	Val	Asn	Val	Leu	Asp	Ser	Asn	Asp	Asn	230	235	240
Ser	Pro	Ala	Phe	Ala	Glu	Ser	Ser	Leu	Ala	Leu	Glu	Ile	Gln	Glu	245	250	255
Asp	Ala	Ala	Pro	Gly	Thr	Leu	Leu	Ile	Lys	Leu	Thr	Ala	Thr	Asp	260	265	270
Pro	Asp	Gln	Gly	Pro	Asn	Gly	Glu	Val	Glu	Phe	Phe	Leu	Ser	Lys	275	280	285
His	Met	Pro	Pro	Glu	Val	Leu	Asp	Thr	Phe	Ser	Ile	Asp	Ala	Lys	290	295	300

Thr Gly Gln Val	Ile Leu Arg Arg Pro	Leu Asp Tyr Glu Lys	Asn
305		310	315
Pro Ala Tyr Glu	Val Asp Val Gln Ala	Arg Asp Leu Gly Pro	Asn
320		325	330
Pro Ile Pro Ala	His Cys Lys Val Leu	Ile Lys Val Leu Asp	Val
335		340	345
Asn Asp Asn Ile	Pro Ser Ile His Val	Thr Trp Ala Ser Gln	Pro
350		355	360
Ser Leu Val Ser	Glu Ala Leu Pro Lys	Asp Ser Phe Ile Ala	Leu
365		370	375
Val Met Ala Asp	Asp Leu Asp Ser Gly	His Asn Gly Leu Val	His
380		385	390
Cys Trp Leu Ser	Gln Glu Leu Gly His	Phe Arg Leu Lys Arg	Thr
395		400	405
Asn Gly Asn Thr	Tyr Met Leu Leu Thr	Asn Ala Thr Leu Asp	Arg
410		415	420
Glu Gln Trp Pro	Lys Tyr Thr Leu Thr	Leu Leu Ala Gln Asp	Gln
425		430	435
Gly Leu Gln Pro	Leu Ser Ala Lys Lys	Gln Leu Ser Ile Gln	Ile
440		445	450
Ser Asp Ile Asn	Asp Asn Ala Pro Val	Phe Glu Lys Ser Arg	Tyr
455		460	465
Glu Val Ser Thr	Arg Glu Asn Asn Leu	Pro Ser Leu His Leu	Ile
470		475	480
Thr Ile Lys Ala	His Asp Ala Asp Leu	Gly Ile Asn Gly Lys	Val
485		490	495
Ser Tyr Arg Ile	Gln Asp Ser Pro Val	Ala His Leu Val Ala	Ile
500		505	510
Asp Ser Asn Thr	Gly Glu Val Thr Ala	Gln Arg Ser Leu Asn	Tyr
515		520	525
Glu Glu Met Ala	Gly Phe Glu Phe Gln	Val Ile Ala Glu Asp	Ser
530		535	540
Gly Gln Pro Met	Leu Ala Ser Ser Val	Ser Val Trp Val Ser	Leu
545		550	555
Leu Asp Ala Asn	Asp Asn Ala Pro Glu	Val Val Gln Pro Val	Leu
560		565	570
Ser Asp Gly Lys	Ala Ser Leu Ser Val	Leu Val Asn Ala Ser	Thr
575		580	585

Gly His Leu Leu Val Pro Ile Glu Thr	Pro Asn Gly Leu Gly Pro
590	595 600
Ala Gly Thr Asp Thr Pro Pro Leu Ala	Thr His Ser Ser Arg Pro
605	610 615
Phe Leu Leu Thr Thr Ile Val Ala Arg	Asp Ala Asp Ser Gly Ala
620	625 630
Asn Gly Glu Pro Leu Tyr Ser Ile Arg	Asn Gly Asn Glu Ala His
635	640 645
Leu Phe Ile Leu Asn Pro His Thr Gly	Gln Leu Phe Val Asn Val
650	655 660
Thr Asn Ala Ser Ser Leu Ile Gly Ser	Glu Trp Glu Leu Glu Ile
665	670 675
Val Val Glu Asp Gln Gly Ser Pro Pro	Leu Gln Thr Arg Ala Leu
680	685 690
Leu Arg Val Met Phe Val Thr Ser Val	Asp His Leu Arg Asp Ser
695	700 705
Ala Arg Lys Pro Gly Ala Leu Ser Met	Ser Met Leu Thr Val Ile
710	715 720
Cys Leu Ala Val Leu Leu Gly Ile Phe	Gly Leu Ile Leu Ala Leu
725	730 735
Phe Met Ser Ile Cys Arg Thr Glu Lys	Lys Asp Asn Arg Ala Tyr
740	745 750
Asn Cys Arg Glu Ala Glu Ser Thr Tyr	Arg Gln Gln Pro Lys Arg
755	760 765
Pro Gln Lys His Ile Gln Lys Ala Asp	Ile His Leu Val Pro Val
770	775 780
Leu Arg Gly Gln Ala Gly Glu Pro Cys	Glu Val Gly Gln Ser His
785	790 795
Lys Asp Val Asp Lys Glu Ala Met Met	Glu Ala Gly Trp Asp Pro
800	805 810
Cys Leu Gln Ala Pro Phe His Leu Thr	Pro Thr Leu Tyr Arg Thr
815	820 825
Leu Arg Asn Gln Gly Asn Gln Gly Ala	Pro Ala Glu Ser Arg Glu
830	835 840
Val Leu Gln Asp Thr Val Asn Leu Leu	Phe Asn His Pro Arg Gln
845	850 855
Arg Asn Ala Ser Arg Glu Asn Leu Asn	Leu Pro Glu Pro Gln Pro
860	865 870

Ala Thr Gly Gln Pro Arg Ser Arg Pro Leu Lys Val Ala Gly Ser	875	880	885
Pro Thr Gly Arg Leu Ala Gly Asp Gln Gly Ser Glu Glu Ala Pro	890	895	900
Gln Arg Pro Pro Ala Ser Ser Ala Thr Leu Arg Arg Gln Arg His	905	910	915
Leu Asn Gly Lys Val Ser Pro Glu Lys Glu Ser Gly Pro Arg Gln	920	925	930
Ile Leu Arg Ser Leu Val Arg Leu Ser Val Ala Ala Phe Ala Glu	935	940	945
Arg Asn Pro Val Glu Glu Leu Thr Val Asp Ser Pro Pro Val Gln	950	955	960
Gln Ile Ser Gln Leu Leu Ser Leu Leu His Gln Gly Gln Phe Gln	965	970	975
Pro Lys Pro Asn His Arg Gly Asn Lys Tyr Leu Ala Lys Pro Gly	980	985	990
Gly Ser Arg Ser Ala Ile Pro Asp Thr Asp Gly Pro Ser Ala Arg	995	1000	1005
Ala Gly Gly Gln Thr Asp Pro Glu Gln Glu Glu Gly Pro Leu Asp	1010	1015	1020
Pro Glu Glu Asp Leu Ser Val Lys Gln Leu Leu Glu Glu Glu Leu	1025	1030	1035
Ser Ser Leu Leu Asp Pro Ser Thr Gly Leu Ala Leu Asp Arg Leu	1040	1045	1050
Ser Ala Pro Asp Pro Ala Trp Met Ala Arg Leu Ser Leu Pro Leu	1055	1060	1065
Thr Thr Asn Tyr Arg Asp Asn Val Ile Ser Pro Asp Ala Ala Ala	1070	1075	1080
Thr Glu Glu Pro Arg Thr Phe Gln Thr Phe Gly Lys Ala Glu Ala	1085	1090	1095
Pro Glu Leu Ser Pro Thr Gly Thr Arg Leu Ala Ser Thr Phe Val	1100	1105	1110
Ser Glu Met Ser Ser Leu Leu Glu Met Leu Leu Glu Gln Arg Ser	1115	1120	1125
Ser Met Pro Val Glu Ala Ala Ser Glu Ala Leu Arg Arg Leu Ser	1130	1135	1140
Val Cys Gly Arg Thr Leu Ser Leu Asp Leu Ala Thr Ser Ala Ala	1145	1150	1155

Ser Gly Met Lys Val Gln Gly Asp Pro Gly Gly Lys Thr Gly Thr  
1160 1165 1170

Glu Gly Lys Ser Arg Gly Ser Ser Ser Ser Arg Cys Leu  
1175 1180

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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 426

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<210> 427

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 427

gtgacgtgga tgcttgggat gttg 24

<210> 428

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 428

tggacacctt cagtattgat gccaaagacag gccaggatcat tctgcgtcga 50

<210> 429

<211> 2037

<212> DNA

<213> Homo sapiens

<400> 429

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ggcctcgggg agtgggaagt ggaggcagga gccttcctta cacttcgcca 150

tgagtttcct catcgactcc agcatcatga ttacctcca gatactatgt 200

tttggatttg ggtggctttt cttcatgcgc caattgttta aagactatga 250

gatacgtcag tatgttgtac aggtgatctt ctccgtgacg tttgcatttt 300



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gatcctgggtt ttcattggtgc ctttttacat tggctatttt attgtgagca 450  
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 tttgccttga gattgactca ttaaaatcag agactgtaac aaaaaaaaaa 1950  
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 ccgccatggc ccaacttggt tattgcagct tataatg 2037

<210> 430

<211> 455

<212> PRT

<213> Homo sapiens

<400> 430

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Leu	Phe	Phe	Gly	Phe	Gly	Trp	Leu	Phe	Phe	Met	Arg	Gln	Leu	Phe
			20						25					30

Lys	Asp	Tyr	Glu	Ile	Arg	Gln	Tyr	Val	Val	Gln	Val	Ile	Phe	Ser
			35						40					45

Val	Thr	Phe	Ala	Phe	Ser	Cys	Thr	Met	Phe	Glu	Leu	Ile	Ile	Phe
			50						55					60

Glu	Ile	Leu	Gly	Val	Leu	Asn	Ser	Ser	Ser	Arg	Tyr	Phe	His	Trp
			65						70					75

Lys	Met	Asn	Leu	Cys	Val	Ile	Leu	Leu	Ile	Leu	Val	Phe	Met	Val
			80						85					90

Pro	Phe	Tyr	Ile	Gly	Tyr	Phe	Ile	Val	Ser	Asn	Ile	Arg	Leu	Leu
			95						100					105

His	Lys	Gln	Arg	Leu	Leu	Phe	Ser	Cys	Leu	Leu	Trp	Leu	Thr	Phe
			110						115					120

Met	Tyr	Phe	Phe	Trp	Lys	Leu	Gly	Asp	Pro	Phe	Pro	Ile	Leu	Ser
			125						130					135

Pro	Lys	His	Gly	Ile	Leu	Ser	Ile	Glu	Gln	Leu	Ile	Ser	Arg	Val
			140						145					150

Gly	Val	Ile	Gly	Val	Thr	Leu	Met	Ala	Leu	Leu	Ser	Gly	Phe	Gly
			155						160					165

Ala	Val	Asn	Cys	Pro	Tyr	Thr	Tyr	Met	Ser	Tyr	Phe	Leu	Arg	Asn
			170						175					180

Val	Thr	Asp	Thr	Asp	Ile	Leu	Ala	Leu	Glu	Arg	Arg	Leu	Leu	Gln
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

	185		190		195
Thr Met Asp Met	Ile Ile Ser Lys Lys	Lys Arg Met Ala Met	Ala		
	200		205		210
Arg Arg Thr Met	Phe Gln Lys Gly Glu	Val His Asn Lys Pro	Ser		
	215		220		225
Gly Phe Trp Gly	Met Ile Lys Ser Val	Thr Thr Ser Ala Ser	Gly		
	230		235		240
Ser Glu Asn Leu	Thr Leu Ile Gln Gln	Glu Val Asp Ala Leu	Glu		
	245		250		255
Glu Leu Ser Arg	Gln Leu Phe Leu Glu	Thr Ala Asp Leu Tyr	Ala		
	260		265		270
Thr Lys Glu Arg	Ile Glu Tyr Ser Lys	Thr Phe Lys Gly Lys	Tyr		
	275		280		285
Phe Asn Phe Leu	Gly Tyr Phe Phe Ser	Ile Tyr Cys Val Trp	Lys		
	290		295		300
Ile Phe Met Ala	Thr Ile Asn Ile Val	Phe Asp Arg Val Gly	Lys		
	305		310		315
Thr Asp Pro Val	Thr Arg Gly Ile Glu	Ile Thr Val Asn Tyr	Leu		
	320		325		330
Gly Ile Gln Phe	Asp Val Lys Phe Trp	Ser Gln His Ile Ser	Phe		
	335		340		345
Ile Leu Val Gly	Ile Ile Ile Val Thr	Ser Ile Arg Gly Leu	Leu		
	350		355		360
Ile Thr Leu Thr	Lys Phe Phe Tyr Ala	Ile Ser Ser Ser Lys	Ser		
	365		370		375
Ser Asn Val Ile	Val Leu Leu Leu Ala	Gln Ile Met Gly Met	Tyr		
	380		385		390
Phe Val Ser Ser	Val Leu Leu Ile Arg	Met Ser Met Pro Leu	Glu		
	395		400		405
Tyr Arg Thr Ile	Ile Thr Glu Val Leu	Gly Glu Leu Gln Phe	Asn		
	410		415		420
Phe Tyr His Arg	Trp Phe Asp Val Ile	Phe Leu Val Ser Ala	Leu		
	425		430		435
Ser Ser Ile Leu	Phe Leu Tyr Leu Ala	His Lys Gln Ala Pro	Glu		
	440		445		450
Lys Gln Met Ala	Pro				
	455				

<210> 431

<211> 407  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 78, 81, 113, 157, 224, 297  
<223> unknown base

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tttccag 407

<210> 432  
<211> 457  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 31, 66, 81-82, 84, 122, 184, 187, 232, 241, 400, 424, 427, 434  
<223> unknown base

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cattctc 457

<210> 433

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 433

aagtggagcc ggagccttcc 20

<210> 434

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 434

tcgttggtta tgcagtagtc gg 22

<210> 435

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 435

attgtttaa gactatgaga tacgtcagta tgttgtacag g 41

<210> 436

<211> 3951

<212> DNA

<213> Homo sapiens

<400> 436

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ttctcacggg ctgtgcctt caatctggac gtgatgggtg cttgctgcaa 150

ggagggcgag ccaggcagcc tcttcggctt ctctgtggcc ctgcaccggc 200

agttgcagcc ccgacccag agctggctgc tgggtgggtgc tccccaggcc 250

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 a 3951

<210> 437

<211> 1141

<212> PRT

<213> Homo sapiens

<400> 437

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				20					25					30
Ala	Val	Ala	Phe	Asn	Leu	Asp	Val	Met	Gly	Ala	Leu	Arg	Lys	Glu
				35					40					45
Gly	Glu	Pro	Gly	Ser	Leu	Phe	Gly	Phe	Ser	Val	Ala	Leu	His	Arg
				50					55					60
Gln	Leu	Gln	Pro	Arg	Pro	Gln	Ser	Trp	Leu	Leu	Val	Gly	Ala	Pro
				65					70					75
Gln	Ala	Leu	Ala	Leu	Pro	Gly	Gln	Gln	Ala	Asn	Arg	Thr	Gly	Gly
				80					85					90
Leu	Phe	Ala	Cys	Pro	Leu	Ser	Leu	Glu	Glu	Thr	Asp	Cys	Tyr	Arg
				95					100					105



Val Asp Ile Asp	Gln Gly Ala Asp Met	Gln Lys Glu Ser Lys Glu	110	115	120
Asn Gln Trp Leu	Gly Val Ser Val Arg	Ser Gln Gly Pro Gly Gly	125	130	135
Lys Ile Val Thr	Cys Ala His Arg Tyr	Glu Ala Arg Gln Arg Val	140	145	150
Asp Gln Ile Leu	Glu Thr Arg Asp Met	Ile Gly Arg Cys Phe Val	155	160	165
Leu Ser Gln Asp	Leu Ala Ile Arg Asp	Glu Leu Asp Gly Gly Glu	170	175	180
Trp Lys Phe Cys	Glu Gly Arg Pro Gln	Gly His Glu Gln Phe Gly	185	190	195
Phe Cys Gln Gln	Gly Thr Ala Ala Ala	Phe Ser Pro Asp Ser His	200	205	210
Tyr Leu Leu Phe	Gly Ala Pro Gly Thr	Tyr Asn Trp Lys Gly Thr	215	220	225
Ala Arg Val Glu	Leu Cys Ala Gln Gly	Ser Ala Asp Leu Ala His	230	235	240
Leu Asp Asp Gly	Pro Tyr Glu Ala Gly	Gly Glu Lys Glu Gln Asp	245	250	255
Pro Arg Leu Ile	Pro Val Pro Ala Asn	Ser Tyr Phe Gly Phe Ser	260	265	270
Ile Asp Ser Gly	Lys Gly Leu Val Arg	Ala Glu Glu Leu Ser Phe	275	280	285
Val Ala Gly Ala	Pro Arg Ala Asn His	Lys Gly Ala Val Val Ile	290	295	300
Leu Arg Lys Asp	Ser Ala Ser Arg Leu	Val Pro Glu Val Met Leu	305	310	315
Ser Gly Glu Arg	Leu Thr Ser Gly Phe	Gly Tyr Ser Leu Ala Val	320	325	330
Ala Asp Leu Asn	Ser Asp Gly Trp Pro	Asp Leu Ile Val Gly Ala	335	340	345
Pro Tyr Phe Phe	Glu Arg Gln Glu Glu	Leu Gly Gly Ala Val Tyr	350	355	360
Val Tyr Leu Asn	Gln Gly Gly His Trp	Ala Gly Ile Ser Pro Leu	365	370	375
Arg Leu Cys Gly	Ser Pro Asp Ser Met	Phe Gly Ile Ser Leu Ala	380	385	390

Val	Leu	Gly	Asp	Leu	Asn	Gln	Asp	Gly	Phe	Pro	Asp	Ile	Ala	Val	395	400	405
Gly	Ala	Pro	Phe	Asp	Gly	Asp	Gly	Lys	Val	Phe	Ile	Tyr	His	Gly	410	415	420
Ser	Ser	Leu	Gly	Val	Val	Ala	Lys	Pro	Ser	Gln	Val	Leu	Glu	Gly	425	430	435
Glu	Ala	Val	Gly	Ile	Lys	Ser	Phe	Gly	Tyr	Ser	Leu	Ser	Gly	Ser	440	445	450
Leu	Asp	Met	Asp	Gly	Asn	Gln	Tyr	Pro	Asp	Leu	Leu	Val	Gly	Ser	455	460	465
Leu	Ala	Asp	Thr	Ala	Val	Leu	Phe	Arg	Ala	Arg	Pro	Ile	Leu	His	470	475	480
Val	Ser	His	Glu	Val	Ser	Ile	Ala	Pro	Arg	Ser	Ile	Asp	Leu	Glu	485	490	495
Gln	Pro	Asn	Cys	Ala	Gly	Gly	His	Ser	Val	Cys	Val	Asp	Leu	Arg	500	505	510
Val	Cys	Phe	Ser	Tyr	Ile	Ala	Val	Pro	Ser	Ser	Tyr	Ser	Pro	Thr	515	520	525
Val	Ala	Leu	Asp	Tyr	Val	Leu	Asp	Ala	Asp	Thr	Asp	Arg	Arg	Leu	530	535	540
Arg	Gly	Gln	Val	Pro	Arg	Val	Thr	Phe	Leu	Ser	Arg	Asn	Leu	Glu	545	550	555
Glu	Pro	Lys	His	Gln	Ala	Ser	Gly	Thr	Val	Trp	Leu	Lys	His	Gln	560	565	570
His	Asp	Arg	Val	Cys	Gly	Asp	Ala	Met	Phe	Gln	Leu	Gln	Glu	Asn	575	580	585
Val	Lys	Asp	Lys	Leu	Arg	Ala	Ile	Val	Val	Thr	Leu	Ser	Tyr	Ser	590	595	600
Leu	Gln	Thr	Pro	Arg	Leu	Arg	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	605	610	615
Pro	Pro	Val	Ala	Pro	Ile	Leu	Asn	Ala	His	Gln	Pro	Ser	Thr	Gln	620	625	630
Arg	Ala	Glu	Ile	His	Phe	Leu	Lys	Gln	Gly	Cys	Gly	Glu	Asp	Lys	635	640	645
Ile	Cys	Gln	Ser	Asn	Leu	Gln	Leu	Val	His	Ala	Arg	Phe	Cys	Thr	650	655	660
Arg	Val	Ser	Asp	Thr	Glu	Phe	Gln	Pro	Leu	Pro	Met	Asp	Val	Asp	665	670	675

Gly Thr Thr Ala	Leu Phe Ala Leu Ser	Gly Gln Pro Val Ile	Gly
	680	685	690
Leu Glu Leu Met	Val Thr Asn Leu Pro	Ser Asp Pro Ala Gln	Pro
	695	700	705
Gln Ala Asp Gly	Asp Asp Ala His Glu	Ala Gln Leu Leu Val	Met
	710	715	720
Leu Pro Asp Ser	Leu His Tyr Ser Gly	Val Arg Ala Leu Asp	Pro
	725	730	735
Ala Glu Lys Pro	Leu Cys Leu Ser Asn	Glu Asn Ala Ser His	Val
	740	745	750
Glu Cys Glu Leu	Gly Asn Pro Met Lys	Arg Gly Ala Gln Val	Thr
	755	760	765
Phe Tyr Leu Ile	Leu Ser Thr Ser Gly	Ile Ser Ile Glu Thr	Thr
	770	775	780
Glu Leu Glu Val	Glu Leu Leu Leu Ala	Thr Ile Ser Glu Gln	Glu
	785	790	795
Leu His Pro Val	Ser Ala Arg Ala Arg	Val Phe Ile Glu Leu	Pro
	800	805	810
Leu Ser Ile Ala	Gly Met Ala Ile Pro	Gln Gln Leu Phe Phe	Ser
	815	820	825
Gly Val Val Arg	Gly Glu Arg Ala Met	Gln Ser Glu Arg Asp	Val
	830	835	840
Gly Ser Lys Val	Lys Tyr Glu Val Thr	Val Ser Asn Gln Gly	Gln
	845	850	855
Ser Leu Arg Thr	Leu Gly Ser Ala Phe	Leu Asn Ile Met Trp	Pro
	860	865	870
His Glu Ile Ala	Asn Gly Lys Trp Leu	Leu Tyr Pro Met Gln	Val
	875	880	885
Glu Leu Glu Gly	Gly Gln Gly Pro Gly	Gln Lys Gly Leu Cys	Ser
	890	895	900
Pro Arg Pro Asn	Ile Leu His Leu Asp	Val Asp Ser Arg Asp	Arg
	905	910	915
Arg Arg Arg Glu	Leu Glu Pro Pro Glu	Gln Gln Glu Pro Gly	Glu
	920	925	930
Arg Gln Glu Pro	Ser Met Ser Trp Trp	Pro Val Ser Ser Ala	Glu
	935	940	945
Lys Lys Lys Asn	Ile Thr Leu Asp Cys	Ala Arg Gly Thr Ala	Asn
	950	955	960

Cys	Val	Val	Phe	Ser	Cys	Pro	Leu	Tyr	Ser	Phe	Asp	Arg	Ala	Ala	
				965					970					975	
Val	Leu	His	Val	Trp	Gly	Arg	Leu	Trp	Asn	Ser	Thr	Phe	Leu	Glu	
				980					985					990	
Glu	Tyr	Ser	Ala	Val	Lys	Ser	Leu	Glu	Val	Ile	Val	Arg	Ala	Asn	
				995					1000					1005	
Ile	Thr	Val	Lys	Ser	Ser	Ile	Lys	Asn	Leu	Met	Leu	Arg	Asp	Ala	
				1010					1015					1020	
Ser	Thr	Val	Ile	Pro	Val	Met	Val	Tyr	Leu	Asp	Pro	Met	Ala	Val	
				1025					1030					1035	
Val	Ala	Glu	Gly	Val	Pro	Trp	Trp	Val	Ile	Leu	Leu	Ala	Val	Leu	
				1040					1045					1050	
Ala	Gly	Leu	Leu	Val	Leu	Ala	Leu	Leu	Val	Leu	Leu	Leu	Trp	Lys	
				1055					1060					1065	
Met	Gly	Phe	Phe	Lys	Arg	Ala	Lys	His	Pro	Glu	Ala	Thr	Val	Pro	
				1070					1075					1080	
Gln	Tyr	His	Ala	Val	Lys	Ile	Pro	Arg	Glu	Asp	Arg	Gln	Gln	Phe	
				1085					1090					1095	
Lys	Glu	Glu	Lys	Thr	Gly	Thr	Ile	Leu	Arg	Asn	Asn	Trp	Gly	Ser	
				1100					1105					1110	
Pro	Arg	Arg	Glu	Gly	Pro	Asp	Ala	His	Pro	Ile	Leu	Ala	Ala	Asp	
				1115					1120					1125	
Gly	His	Pro	Glu	Leu	Gly	Pro	Asp	Gly	His	Pro	Gly	Pro	Gly	Thr	
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Ala

<210> 438

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 438

ggctgacacc gcagtgtctt tcag 24

<210> 439

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 439  
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<210> 440  
<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 440  
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<210> 441  
<211> 1964  
<212> DNA  
<213> Homo sapiens

<400> 441  
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ggagctgcga gcacagtgtt ggctcacaac aagatgctca aggtgtcagc 150  
cgtactgtgt gtgtgtgcag ccgcttggtg cagtcagtct ctgcgagctg 200  
ccgcggcggg ggctgcagcc ggggggcggg cggacggcgg taattttctg 250  
gatgataaac aatggctcac cacaatctct cagtatgaca aggaagtcgg 300  
acagtggaac aaattccgag acgaagtaga ggatgattat ttccgcactt 350  
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<210> 442

<211> 436

<212> PRT

<213> Homo sapiens

<400> 442

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				20				25						30
Gly	Arg	Ser	Asp	Gly	Gly	Asn	Phe	Leu	Asp	Asp	Lys	Gln	Trp	Leu

35										40					45				
Thr	Thr	Ile	Ser	Gln	Tyr	Asp	Lys	Glu	Val	Gly	Gln	Trp	Asn	Lys					
				50					55					60					
Phe	Arg	Asp	Glu	Val	Glu	Asp	Asp	Tyr	Phe	Arg	Thr	Trp	Ser	Pro					
				65					70					75					
Gly	Lys	Pro	Phe	Asp	Gln	Ala	Leu	Asp	Pro	Ala	Lys	Asp	Pro	Cys					
				80					85					90					
Leu	Lys	Met	Lys	Cys	Ser	Arg	His	Lys	Val	Cys	Ile	Ala	Gln	Asp					
				95					100					105					
Ser	Gln	Thr	Ala	Val	Cys	Ile	Ser	His	Arg	Arg	Leu	Thr	His	Arg					
				110					115					120					
Met	Lys	Glu	Ala	Gly	Val	Asp	His	Arg	Gln	Trp	Arg	Gly	Pro	Ile					
				125					130					135					
Leu	Ser	Thr	Cys	Lys	Gln	Cys	Pro	Val	Val	Tyr	Pro	Ser	Pro	Val					
				140					145					150					
Cys	Gly	Ser	Asp	Gly	His	Thr	Tyr	Ser	Phe	Gln	Cys	Lys	Leu	Glu					
				155					160					165					
Tyr	Gln	Ala	Cys	Val	Leu	Gly	Lys	Gln	Ile	Ser	Val	Lys	Cys	Glu					
				170					175					180					
Gly	His	Cys	Pro	Cys	Pro	Ser	Asp	Lys	Pro	Thr	Ser	Thr	Ser	Arg					
				185					190					195					
Asn	Val	Lys	Arg	Ala	Cys	Ser	Asp	Leu	Glu	Phe	Arg	Glu	Val	Ala					
				200					205					210					
Asn	Arg	Leu	Arg	Asp	Trp	Phe	Lys	Ala	Leu	His	Glu	Ser	Gly	Ser					
				215					220					225					
Gln	Asn	Lys	Lys	Thr	Lys	Thr	Leu	Leu	Arg	Pro	Glu	Arg	Ser	Arg					
				230					235					240					
Phe	Asp	Thr	Ser	Ile	Leu	Pro	Ile	Cys	Lys	Asp	Ser	Leu	Gly	Trp					
				245					250					255					
Met	Phe	Asn	Arg	Leu	Asp	Thr	Asn	Tyr	Asp	Leu	Leu	Leu	Asp	Gln					
				260					265					270					
Ser	Glu	Leu	Arg	Ser	Ile	Tyr	Leu	Asp	Lys	Asn	Glu	Gln	Cys	Thr					
				275					280					285					
Lys	Ala	Phe	Phe	Asn	Ser	Cys	Asp	Thr	Tyr	Lys	Asp	Ser	Leu	Ile					
				290					295					300					
Ser	Asn	Asn	Glu	Trp	Cys	Tyr	Cys	Phe	Gln	Arg	Gln	Gln	Asp	Pro					
				305					310					315					
Pro	Cys	Gln	Thr	Glu	Leu	Ser	Asn	Ile	Gln	Lys	Arg	Gln	Gly	Val					

	320		325		330
Lys Lys Leu Leu Gly Gln Tyr Ile Pro	335	Leu Cys Asp Glu Asp Gly	340		345
Tyr Tyr Lys Pro Thr Gln Cys His Gly	350	Ser Val Gly Gln Cys Trp	355		360
Cys Val Asp Arg Tyr Gly Asn Glu Val	365	Met Gly Ser Arg Ile Asn	370		375
Gly Val Ala Asp Cys Ala Ile Asp Phe	380	Glu Ile Ser Gly Asp Phe	385		390
Ala Ser Gly Asp Phe His Glu Trp Thr	395	Asp Asp Glu Asp Asp Glu	400		405
Asp Asp Ile Met Asn Asp Glu Asp Glu	410	Ile Glu Asp Asp Asp Glu	415		420
Asp Glu Gly Asp Asp Asp Asp Gly Gly	425	Asp Asp His Asp Val Tyr	430		435

Ile

<210> 443

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 443

cagcaatatt cagaagcggc aaggg 25

<210> 444

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 444

catcatggtc atcaccacca tcatcatc 28

<210> 445

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 445



ggttactaca agccaacaca atgtcatggc agtgttggac agtgctgg 48

<210> 446

<211> 3617

<212> DNA

<213> Homo sapiens

<400> 446

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cagggatggg cgacaagatc tggctgcctt tccccgtgct ccttctggcc 150  
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taagtttatt tttaatagta tctgtcaagt taatatctgt caacagttaa 1650  
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agaatttaga aaaacttgag aaaacctaata ccaaaataaa attcacttaa 1850  
gtagaactat aaataaatat ctagaatctg actggctcat catgacatcc 1900  
tactcataac ataaatcaaa ggagatgatt aatttccagt tagctggaag 1950  
aaactttggc tgtaggtttt tattttctac aagaattctg gtttgaatta 2000  
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taaaatggcc tttctgaaca ctttatttat tgatgttgaa gtaaggatta 2150  
gaaacataga ctcccaagtt ttaaacacct aaatgtgaat aacccatata 2200  
tacaacaaag tttctgccat ctagcttttt gaagtctatg ggggtcttac 2250  
tcaagtacta gtaatttaac ttcattcatga atgaactata atttttaagt 2300  
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 cataaccaa aaagcaaaac ttgtaaacag agtaaaaatc tttaatatct 3050  
 ctaaagacat actgtttatc tgcttcatat gcttttttta atttcactat 3100  
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<210> 447

<211> 229

<212> PRT

<213> Homo sapiens

<400> 447

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Ala	Leu	Pro	Pro	Val	Leu	Leu	Pro	Gly	Ala	Ala	Gly	Phe	Thr	Pro
				20					25					30

Ser	Leu	Asp	Ser	Asp	Phe	Thr	Phe	Thr	Leu	Pro	Ala	Gly	Gln	Lys
				35					40					45

Glu	Cys	Phe	Tyr	Gln	Pro	Met	Pro	Leu	Lys	Ala	Ser	Leu	Glu	Ile
				50					55					60

Glu Tyr Gln Val	Leu Asp Gly Ala Gly	Leu Asp Ile Asp Phe His
	65	70 75
Leu Ala Ser Pro	Glu Gly Lys Thr Leu Val Phe Glu Gln Arg Lys	
	80	85 90
Ser Asp Gly Val	His Thr Val Glu Thr Glu Val Gly Asp Tyr Met	
	95	100 105
Phe Cys Phe Asp	Asn Thr Phe Ser Thr Ile Ser Glu Lys Val Ile	
	110	115 120
Phe Phe Glu Leu	Ile Leu Asp Asn Met Gly Glu Gln Ala Gln Glu	
	125	130 135
Gln Glu Asp Trp	Lys Lys Tyr Ile Thr Gly Thr Asp Ile Leu Asp	
	140	145 150
Met Lys Leu Glu	Asp Ile Leu Glu Ser Ile Asn Ser Ile Lys Ser	
	155	160 165
Arg Leu Ser Lys	Ser Gly His Ile Gln Ile Leu Leu Arg Ala Phe	
	170	175 180
Glu Ala Arg Asp	Arg Asn Ile Gln Glu Ser Asn Phe Asp Arg Val	
	185	190 195
Asn Phe Trp Ser	Met Val Asn Leu Val Val Met Val Val Val Ser	
	200	205 210
Ala Ile Gln Val	Tyr Met Leu Lys Ser Leu Phe Glu Asp Lys Arg	
	215	220 225
Lys Ser Arg Thr		

<210> 448  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 448  
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<210> 449  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 449

gtcttccagt ttcatatcca ata 23

<210> 450

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 450

ccagaaggag cacggggaag ggcagccaga tcttgctgcc cat 43

<210> 451

<211> 859

<212> DNA

<213> Homo sapiens

<400> 451

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gccctgcca gtgtgtcctg gatgctgctt tctgcctca ttctcctgtg 150  
tcaggttcaa ggtgaagaaa ccagaagga actgccctct ccacggatca 200  
gctgtcccaa aggctccaag gcctatggct cccctgcta tgccttgttt 250  
ttgtcaccaa aatcctggat ggatgcagat ctggcttgcc agaagcggcc 300  
ctctggaaaa ctggtgtctg tgctcagtgg ggctgaggga tccttcgtgt 350  
cctccctggt gaggagcatt agtaacagct actcatacat ctggattggg 400  
ctccatgacc ccacacaggg ctctgagcct gatggagatg gatgggagtg 450  
gagtagcact gatgtgatga attactttgc atgggagaaa aatccctcca 500  
ccatcttaaa ccctggccac tgtgggagcc tgtcaagaag cacaggattt 550  
ctgaagtgga aagattataa ctgtgatgca aagttaccct atgtctgcaa 600  
gttcaaggac tagggcaggt ggggaagtcag cagcctcagc ttggcgtgca 650  
gctcatcatg gacatgagac cagtgtgaag actcaccctg gaagagaata 700  
ttctcccaa actgccctac ctgactacct tgtcatgac ctcttctttt 750  
ttcttttttc ttcaccttca tttcaggctt ttctctgtct tccatgtctt 800  
gagatctcag agaataataa taaaatgtt actttataaa aaaaaaaaaa 850  
aaaaaaaaa 859

<210> 452

<211> 175

<212> PRT  
<213> Homo sapiens

<400> 452  
Met Leu Pro Pro Met Ala Leu Pro Ser Val Ser Trp Met Leu Leu  
1 5 10 15  
Ser Cys Leu Ile Leu Leu Cys Gln Val Gln Gly Glu Glu Thr Gln  
20 25 30  
Lys Glu Leu Pro Ser Pro Arg Ile Ser Cys Pro Lys Gly Ser Lys  
35 40 45  
Ala Tyr Gly Ser Pro Cys Tyr Ala Leu Phe Leu Ser Pro Lys Ser  
50 55 60  
Trp Met Asp Ala Asp Leu Ala Cys Gln Lys Arg Pro Ser Gly Lys  
65 70 75  
Leu Val Ser Val Leu Ser Gly Ala Glu Gly Ser Phe Val Ser Ser  
80 85 90  
Leu Val Arg Ser Ile Ser Asn Ser Tyr Ser Tyr Ile Trp Ile Gly  
95 100 105  
Leu His Asp Pro Thr Gln Gly Ser Glu Pro Asp Gly Asp Gly Trp  
110 115 120  
Glu Trp Ser Ser Thr Asp Val Met Asn Tyr Phe Ala Trp Glu Lys  
125 130 135  
Asn Pro Ser Thr Ile Leu Asn Pro Gly His Cys Gly Ser Leu Ser  
140 145 150  
Arg Ser Thr Gly Phe Leu Lys Trp Lys Asp Tyr Asn Cys Asp Ala  
155 160 165  
Lys Leu Pro Tyr Val Cys Lys Phe Lys Asp  
170 175

<210> 453  
<211> 550  
<212> DNA  
<213> Homo sapiens

<400> 453  
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tggggtgaga gcacagagga gtggggccggg accatgcggg ggacgcggct 100  
ggcgctcctg gcgctggtgc tggctgcctg cggagagctg gcgccggccc 150  
tgcgctgcta cgtctgtccg gagcccacag gagtgtcgga ctgtgtcacc 200  
atcgccacct gcaccaccaa cgaaaccatg tgcaagacca cactctactc 250  
ccgggagata gtgtaccct tccaggggga ctccacggtg accaagtcct 300

gtgccagcaa gtgtaagccc tcggatgtgg atggcatcgg ccagaccctg 350  
cccgtgtcct gctgcaatac tgagctgtgc aatgtagacg gggcgcccg 400  
tctgaacagc ctccactgcg gggccctcac gctcctccca ctcttgagcc 450  
tccgactgta gagtccccgc ccacccccat ggccctatgc ggcccagccc 500  
cgaatgcctt gaagaagtgc cccctgcacc aggaaaaaaa aaaaaaaaaa 550

<210> 454  
<211> 125  
<212> PRT  
<213> Homo sapiens

<400> 454  
Met Arg Gly Thr Arg Leu Ala Leu Leu Ala Leu Val Leu Ala Ala  
1 5 10 15  
Cys Gly Glu Leu Ala Pro Ala Leu Arg Cys Tyr Val Cys Pro Glu  
20 25 30  
Pro Thr Gly Val Ser Asp Cys Val Thr Ile Ala Thr Cys Thr Thr  
35 40 45  
Asn Glu Thr Met Cys Lys Thr Thr Leu Tyr Ser Arg Glu Ile Val  
50 55 60  
Tyr Pro Phe Gln Gly Asp Ser Thr Val Thr Lys Ser Cys Ala Ser  
65 70 75  
Lys Cys Lys Pro Ser Asp Val Asp Gly Ile Gly Gln Thr Leu Pro  
80 85 90  
Val Ser Cys Cys Asn Thr Glu Leu Cys Asn Val Asp Gly Ala Pro  
95 100 105  
Ala Leu Asn Ser Leu His Cys Gly Ala Leu Thr Leu Leu Pro Leu  
110 115 120  
Leu Ser Leu Arg Leu  
125

<210> 455  
<211> 1518  
<212> DNA  
<213> Homo sapiens

<400> 455  
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agccgaaccg gcacggtttc gtggggaccc aggcttgcaa agtgacggtc 100  
attttctctt tctttctccc tcttgagtcc ttctgagatg atggctcttg 150  
gcgcagcggg agctacccgg gtctttgtcg cgatggtagc ggcggctctc 200

ggcgccacc ctctgctggg agtgagcgcc accttgaact cggttctcaa 250  
 ttccaacgct atcaagaacc tgccccacc gctggggcgc gctgcggggc 300  
 acccaggctc tgcagtcagc gccgcgccgg gaatcctgta cccgggcggg 350  
 aataagtacc agaccattga caactaccag ccgtaccctg gcgcagagga 400  
 cgaggagtgc ggactgatg agtactgcgc tagtcccacc cgcggagggg 450  
 acgcaggcgt gcaaatctgt ctgcctgca ggaagcgccg aaaacgctgc 500  
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 tgtgtcttct gatcaaaatc atttccgagg agaaattgag gaaaccatca 600  
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 accaccttgt cttcaaaaat gtatcacacc aaaggacaag aaggttctgt 700  
 ttgtctccgg tcatcagact gtgcctcagg attgtgttgt gctagacact 750  
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 aagcatagga gaaaaggctc tcatggacta gaaatattcc agcgttggtta 850  
 ctgtggagaa ggtctgtctt gccggataca gaaagatcac catcaagcca 900  
 gtaattcttc taggcttcac acttgtcaga gacactaaac cagctatcca 950  
 aatgcagtga actcctttta tataatagat gctatgaaaa ccttttatga 1000  
 ccttcatcaa ctcaatccta aggatataca agttctgtgg tttcagttaa 1050  
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 ttatggaact ccctgtgat tgcagtaaatt tactgtattg taaattctca 1150  
 gtgtggcact tacctgtaaa tgcaatgaaa cttttaatta tttttctaaa 1200  
 ggtgctgcac tgccatttt tctcttggt atgtaaattt ttgtacacat 1250  
 tgattgttat cttgactgac aaatattcta tattgaactg aagtaaata 1300  
 tttcagctta tagttcttaa aagcataacc ctttacccta ttttaattcta 1350  
 gagtctagaa cgcaaggatc tcttggaatg acaaatgata ggtacctaaa 1400  
 atgtaacatg aaaatactag cttatcttct gaaatgtact atcttaatgc 1450  
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 catttaaaaa aaaaaaaaa 1518

<210> 456

<211> 266



<212> PRT  
<213> Homo sapiens

<400> 456

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				20					25					30
Ala	Thr	Leu	Asn	Ser	Val	Leu	Asn	Ser	Asn	Ala	Ile	Lys	Asn	Leu
				35					40					45
Pro	Pro	Pro	Leu	Gly	Gly	Ala	Ala	Gly	His	Pro	Gly	Ser	Ala	Val
				50					55					60
Ser	Ala	Ala	Pro	Gly	Ile	Leu	Tyr	Pro	Gly	Gly	Asn	Lys	Tyr	Gln
				65					70					75
Thr	Ile	Asp	Asn	Tyr	Gln	Pro	Tyr	Pro	Cys	Ala	Glu	Asp	Glu	Glu
				80					85					90
Cys	Gly	Thr	Asp	Glu	Tyr	Cys	Ala	Ser	Pro	Thr	Arg	Gly	Gly	Asp
				95					100					105
Ala	Gly	Val	Gln	Ile	Cys	Leu	Ala	Cys	Arg	Lys	Arg	Arg	Lys	Arg
				110					115					120
Cys	Met	Arg	His	Ala	Met	Cys	Cys	Pro	Gly	Asn	Tyr	Cys	Lys	Asn
				125					130					135
Gly	Ile	Cys	Val	Ser	Ser	Asp	Gln	Asn	His	Phe	Arg	Gly	Glu	Ile
				140					145					150
Glu	Glu	Thr	Ile	Thr	Glu	Ser	Phe	Gly	Asn	Asp	His	Ser	Thr	Leu
				155					160					165
Asp	Gly	Tyr	Ser	Arg	Arg	Thr	Thr	Leu	Ser	Ser	Lys	Met	Tyr	His
				170					175					180
Thr	Lys	Gly	Gln	Glu	Gly	Ser	Val	Cys	Leu	Arg	Ser	Ser	Asp	Cys
				185					190					195
Ala	Ser	Gly	Leu	Cys	Cys	Ala	Arg	His	Phe	Trp	Ser	Lys	Ile	Cys
				200					205					210
Lys	Pro	Val	Leu	Lys	Glu	Gly	Gln	Val	Cys	Thr	Lys	His	Arg	Arg
				215					220					225
Lys	Gly	Ser	His	Gly	Leu	Glu	Ile	Phe	Gln	Arg	Cys	Tyr	Cys	Gly
				230					235					240
Glu	Gly	Leu	Ser	Cys	Arg	Ile	Gln	Lys	Asp	His	His	Gln	Ala	Ser
				245					250					255
Asn	Ser	Ser	Arg	Leu	His	Thr	Cys	Gln	Arg	His				
				260					265					

<210> 457  
<211> 638  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 30, 123, 133, 139, 180, 214, 259, 282, 308, 452, 467, 471, 473,  
509, 556  
<223> unknown base

<400> 457  
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gcgcagcggg agctaaccgc gttttttgtg gcgatggtag cggcggtttt 200  
  
cggcggccac ctntgtctgg gactgagcgc caccttgaat cggttttcaa 250  
  
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aataagtacc agaccattga caattaccag ccgtaccgt gcgcagagga 400  
  
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angcgggcgt gcaaatntgt ntngcctgca ggaagcgcg aaaacgctgc 500  
  
atgcgtcang ctatgtgctg ccccggaat tactgcaaaa atggaatatg 550  
  
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ctgaaagctt tggtaatgat catagcacct tggatggg 638

<210> 458  
<211> 4040  
<212> DNA  
<213> Homo sapiens

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ttctctcctg cacgcggtgc ttgggctcgg ccaggcgggg tccgccgcca 150  
  
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gtatatTTTT gtggaatgaa aaggaagtat tagaaatgag ctgaagacca 250  
  
ttcacagatt aatatttttg gggacagatt tgtgatgctt gattcaccct 300

tgaagtaatg tagacagaag ttctcaaatt tgcatattac atcaactgga 350  
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agaatgggag tctgggttaa taaagatgac tatatcagag acttgaaaag 450  
gatcattctc tgttttctga tagtgatatat ggccatttta gtgggcacag 500  
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ggagaaaagg gacttgagga taatcaaggt ggccagtatg aaagctggaa 750  
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tggaactct ccgaaatcaa ggcaagagga ataaggatga actttgataa 2650  
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catcatgtat tctttgttat ttgcttttaa caaccttaa aaaatattaa 2950  
aacgattctt agctcagagc catacaaaag taggctggat tcagtccatg 3000  
gaccatagat tgctgtcccc ctgcacggac ttataatgtt tcaggtggct 3050  
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tagtttttgg tcacttggtc tcctaaaaat gctatcccta accatatatt 3200  
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gtatatgtgc acacagtaag tacacaaatt tgagcaacag taagtgcaca 3400  
aattctgtag tttgctgtat catccaggaa aacctgaggg aaaaaaatta 3450  
tagcaattaa ctgggcattg tagagtatcc taaatatggt atcaagtatt 3500  
tagagttcta tattttaaag atatatgtgt tcatgtattt tctgaaattg 3550  
ctttcataga aattttccca ctgatatgtg atttttgagg catctaatat 3600  
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aatgatactg tagttattcc agttactagt ttactgtcag agggctgcct 3800  
ttttcagata aatattgaca taataactga agttattttt ataagaaaat 3850  
caagtatata aatctaggaa agggatcttc tagtttctgt gttgtttaga 3900  
ctcaaagaat cacaaatttg tcagtaacat gtagttgttt agttataatt 3950  
cagagtgtac agaatggtaa aaattccaat cagtcaaaag aggtcaatga 4000  
attaaaaggc ttgcaacttt ttcaaaaaaa aaaaaaaaaa 4040

<210> 459

<211> 747

<212> PRT

<213> Homo sapiens

<400> 459

Met	Gly	Val	Trp	Leu	Asn	Lys	Asp	Asp	Tyr	Ile	Arg	Asp	Leu	Lys
1				5					10					15
Arg	Ile	Ile	Leu	Cys	Phe	Leu	Ile	Val	Tyr	Met	Ala	Ile	Leu	Val
				20					25					30
Gly	Thr	Asp	Gln	Asp	Phe	Tyr	Ser	Leu	Leu	Gly	Val	Ser	Lys	Thr
				35					40					45
Ala	Ser	Ser	Arg	Glu	Ile	Arg	Gln	Ala	Phe	Lys	Lys	Leu	Ala	Leu
				50					55					60
Lys	Leu	His	Pro	Asp	Lys	Asn	Pro	Asn	Asn	Pro	Asn	Ala	His	Gly
				65					70					75

Asp	Phe	Leu	Lys	Ile	Asn	Arg	Ala	Tyr	Glu	Val	Leu	Lys	Asp	Glu	80	85	90
Asp	Leu	Arg	Lys	Lys	Tyr	Asp	Lys	Tyr	Gly	Glu	Lys	Gly	Leu	Glu	95	100	105
Asp	Asn	Gln	Gly	Gly	Gln	Tyr	Glu	Ser	Trp	Asn	Tyr	Tyr	Arg	Tyr	110	115	120
Asp	Phe	Gly	Ile	Tyr	Asp	Asp	Asp	Pro	Glu	Ile	Ile	Thr	Leu	Glu	125	130	135
Arg	Arg	Glu	Phe	Asp	Ala	Ala	Val	Asn	Ser	Gly	Glu	Leu	Trp	Phe	140	145	150
Val	Asn	Phe	Tyr	Ser	Pro	Gly	Cys	Ser	His	Cys	His	Asp	Leu	Ala	155	160	165
Pro	Thr	Trp	Arg	Asp	Phe	Ala	Lys	Glu	Val	Asp	Gly	Leu	Leu	Arg	170	175	180
Ile	Gly	Ala	Val	Asn	Cys	Gly	Asp	Asp	Arg	Met	Leu	Cys	Arg	Met	185	190	195
Lys	Gly	Val	Asn	Ser	Tyr	Pro	Ser	Leu	Phe	Ile	Phe	Arg	Ser	Gly	200	205	210
Met	Ala	Pro	Val	Lys	Tyr	His	Gly	Asp	Arg	Ser	Lys	Glu	Ser	Leu	215	220	225
Val	Ser	Phe	Ala	Met	Gln	His	Val	Arg	Ser	Thr	Val	Thr	Glu	Leu	230	235	240
Trp	Thr	Gly	Asn	Phe	Val	Asn	Ser	Ile	Gln	Thr	Ala	Phe	Ala	Ala	245	250	255
Gly	Ile	Gly	Trp	Leu	Ile	Thr	Phe	Cys	Ser	Lys	Gly	Gly	Asp	Cys	260	265	270
Leu	Thr	Ser	Gln	Thr	Arg	Leu	Arg	Leu	Ser	Gly	Met	Leu	Phe	Leu	275	280	285
Asn	Ser	Leu	Asp	Ala	Lys	Glu	Ile	Tyr	Leu	Glu	Val	Ile	His	Asn	290	295	300
Leu	Pro	Asp	Phe	Glu	Leu	Leu	Ser	Ala	Asn	Thr	Leu	Glu	Asp	Arg	305	310	315
Leu	Ala	His	His	Arg	Trp	Leu	Leu	Phe	Phe	His	Phe	Gly	Lys	Asn	320	325	330
Glu	Asn	Ser	Asn	Asp	Pro	Glu	Leu	Lys	Lys	Leu	Lys	Thr	Leu	Leu	335	340	345
Lys	Asn	Asp	His	Ile	Gln	Val	Gly	Arg	Phe	Asp	Cys	Ser	Ser	Ala	350	355	360

Pro	Asp	Ile	Cys	Ser	Asn	Leu	Tyr	Val	Phe	Gln	Pro	Ser	Leu	Ala	365	370	375
Val	Phe	Lys	Gly	Gln	Gly	Thr	Lys	Glu	Tyr	Glu	Ile	His	His	Gly	380	385	390
Lys	Lys	Ile	Leu	Tyr	Asp	Ile	Leu	Ala	Phe	Ala	Lys	Glu	Ser	Val	395	400	405
Asn	Ser	His	Val	Thr	Thr	Leu	Gly	Pro	Gln	Asn	Phe	Pro	Ala	Asn	410	415	420
Asp	Lys	Glu	Pro	Trp	Leu	Val	Asp	Phe	Phe	Ala	Pro	Trp	Cys	Pro	425	430	435
Pro	Cys	Arg	Ala	Leu	Leu	Pro	Glu	Leu	Arg	Arg	Ala	Ser	Asn	Leu	440	445	450
Leu	Tyr	Gly	Gln	Leu	Lys	Phe	Gly	Thr	Leu	Asp	Cys	Thr	Val	His	455	460	465
Glu	Gly	Leu	Cys	Asn	Met	Tyr	Asn	Ile	Gln	Ala	Tyr	Pro	Thr	Thr	470	475	480
Val	Val	Phe	Asn	Gln	Ser	Asn	Ile	His	Glu	Tyr	Glu	Gly	His	His	485	490	495
Ser	Ala	Glu	Gln	Ile	Leu	Glu	Phe	Ile	Glu	Asp	Leu	Met	Asn	Pro	500	505	510
Ser	Val	Val	Ser	Leu	Thr	Pro	Thr	Thr	Phe	Asn	Glu	Leu	Val	Thr	515	520	525
Gln	Arg	Lys	His	Asn	Glu	Val	Trp	Met	Val	Asp	Phe	Tyr	Ser	Pro	530	535	540
Trp	Cys	His	Pro	Cys	Gln	Val	Leu	Met	Pro	Glu	Trp	Lys	Arg	Met	545	550	555
Ala	Arg	Thr	Leu	Thr	Gly	Leu	Ile	Asn	Val	Gly	Ser	Ile	Asp	Cys	560	565	570
Gln	Gln	Tyr	His	Ser	Phe	Cys	Ala	Gln	Glu	Asn	Val	Gln	Arg	Tyr	575	580	585
Pro	Glu	Ile	Arg	Phe	Phe	Pro	Pro	Lys	Ser	Asn	Lys	Ala	Tyr	Gln	590	595	600
Tyr	His	Ser	Tyr	Asn	Gly	Trp	Asn	Arg	Asp	Ala	Tyr	Ser	Leu	Arg	605	610	615
Ile	Trp	Gly	Leu	Gly	Phe	Leu	Pro	Gln	Val	Ser	Thr	Asp	Leu	Thr	620	625	630
Pro	Gln	Thr	Phe	Ser	Glu	Lys	Val	Leu	Gln	Gly	Lys	Asn	His	Trp	635	640	645

Val	Ile	Asp	Phe	Tyr	Ala	Pro	Trp	Cys	Gly	Pro	Cys	Gln	Asn	Phe
				650					655					660
Ala	Pro	Glu	Phe	Glu	Leu	Leu	Ala	Arg	Met	Ile	Lys	Gly	Lys	Val
				665					670					675
Lys	Ala	Gly	Lys	Val	Asp	Cys	Gln	Ala	Tyr	Ala	Gln	Thr	Cys	Gln
				680					685					690
Lys	Ala	Gly	Ile	Arg	Ala	Tyr	Pro	Thr	Val	Lys	Phe	Tyr	Phe	Tyr
				695					700					705
Glu	Arg	Ala	Lys	Arg	Asn	Phe	Gln	Glu	Glu	Gln	Ile	Asn	Thr	Arg
				710					715					720
Asp	Ala	Lys	Ala	Ile	Ala	Ala	Leu	Ile	Ser	Glu	Lys	Leu	Glu	Thr
				725					730					735
Leu	Arg	Asn	Gln	Gly	Lys	Arg	Asn	Lys	Asp	Glu	Leu			
				740					745					

<210> 460

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 460

actccccagg ctgttcacac tgcc 24

<210> 461

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 461

gatcagccag ccaataccag cagc 24

<210> 462

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 462

gtgggtgatga tagaatgctt tgccgaatga aaggagtcaa cagctatccc 50

<210> 463

<211> 1818

<212> DNA



<213> Homo sapiens

<400> 463

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ggacagagca aagccatgaa catcatccta gaaatccttc tgcttctgat 100
caccatcatc tactcctact tggagtcggt ggtgaagttt ttcattcctc 150
agaggagaaa atctgtggct ggggagattg ttctcattac tggagctggg 200
catggaatag gcaggcagac tacttatgaa ttgcaaaac gacagagcat 250
attggttctg tgggatatta ataagcgcgg tgtggaggaa actgcagctg 300
agtgccgaaa actaggcgtc actgcgcatg cgtatgtggg agactgcagc 350
aacagagaag agatctatcg ctctctaaat cagggtgaaga aagaagtggg 400
tgatgtaaca atcgtggtga ataatgctgg gacagtatat ccagccgata 450
ttctcagcac caaggatgaa gagattacca agacatttga ggtcaacatc 500
ctaggacatt tttggatcac aaaagcactt cttccatcga tgatggagag 550
aaatcatggc cacatcgtca cagtggcttc agtgtgcggc cacgaaggga 600
ttccttacct catcccatat tgttccagea aatttgccgc tgttggtttt 650
cacagaggtc tgacatcaga acttcaggcc ttgggaaaaa ctggtatcaa 700
aacctcatgt ctctgccag tttttgtgaa tactgggttc accaaaaatc 750
caagcacaag attatggcct gtattggaga cagatgaagt cgtaagaagt 800
ctgatagatg gaatacttac caataagaaa atgatttttg ttccatcgta 850
tatcaatatc tttctgagac tacagaagtt tcttcttgaa cgcgcctcag 900
cgatttttaa tcgtatgcag aatattcaat ttgaagcagt ggttggccac 950
aaaatcaaaa tgaaatgaat aaataagctc cagccagaga tgtatgcatg 1000
ataatgatat gaatagtttc gaatcaatgc tgcaaagctt tatttcacat 1050
tttttcagtc ctgataatat taaaaacatt ggtttggcac tagcagcagt 1100
caaacgaaca agattaatta cctgtcttcc tgtttctcaa gaatatttac 1150
gtagtttttc ataggtctgt ttttctttc atgcctctta aaaacttctg 1200
tgcttacata aacatactta aaagggtttc tttaagatat tttatttttc 1250
catttaaagg tggacaaaag ctacctccct aaaagtaaat acaaagagaa 1300
cttatttaca caggggaagg ttaagactgt tcaagtagca ttccaatctg 1350
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tagccatgcc acagaatata aacaagaaca cagaatgagt gcacagctaa 1400  
gagatcaagt ttcagcaggc agctttatct caacctggac atattttaag 1450  
attcagcatt tgaaagattt ccctagcctc ttcctttttc attagcccaa 1500  
aacggtgcaa ctctattctg gactttatta ctigattctg tcttctgtat 1550  
aactctgaag tccacaaaaa gtggaccctc tatatttcct ccctttttat 1600  
agtcttataa gatacattat gaaaggtgac cgactctatt ttaaacttca 1650  
gaattttaag ttctagcccc atgataacct ttttctttgt aatttatgct 1700  
ttcatatata cttaggtccca gagatgttta gacaatttta ggctcaaaaa 1750  
ttaaagctaa cacaggaaaa ggaactgtac tggctattac ataagaaaca 1800  
atggacccaa gagaagaa 1818

<210> 464  
<211> 300  
<212> PRT  
<213> Homo sapiens

<400> 464  
Met Asn Ile Ile Leu Glu Ile Leu Leu Leu Leu Ile Thr Ile Ile  
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Tyr Ser Tyr Leu Glu Ser Leu Val Lys Phe Phe Ile Pro Gln Arg  
20 25 30  
Arg Lys Ser Val Ala Gly Glu Ile Val Leu Ile Thr Gly Ala Gly  
35 40 45  
His Gly Ile Gly Arg Gln Thr Thr Tyr Glu Phe Ala Lys Arg Gln  
50 55 60  
Ser Ile Leu Val Leu Trp Asp Ile Asn Lys Arg Gly Val Glu Glu  
65 70 75  
Thr Ala Ala Glu Cys Arg Lys Leu Gly Val Thr Ala His Ala Tyr  
80 85 90  
Val Val Asp Cys Ser Asn Arg Glu Glu Ile Tyr Arg Ser Leu Asn  
95 100 105  
Gln Val Lys Lys Glu Val Gly Asp Val Thr Ile Val Val Asn Asn  
110 115 120  
Ala Gly Thr Val Tyr Pro Ala Asp Leu Leu Ser Thr Lys Asp Glu  
125 130 135  
Glu Ile Thr Lys Thr Phe Glu Val Asn Ile Leu Gly His Phe Trp  
140 145 150  
Ile Thr Lys Ala Leu Leu Pro Ser Met Met Glu Arg Asn His Gly

155										160					165				
His	Ile	Val	Thr	Val	Ala	Ser	Val	Cys	Gly	His	Glu	Gly	Ile	Pro					
				170					175					180					
Tyr	Leu	Ile	Pro	Tyr	Cys	Ser	Ser	Lys	Phe	Ala	Ala	Val	Gly	Phe					
				185					190					195					
His	Arg	Gly	Leu	Thr	Ser	Glu	Leu	Gln	Ala	Leu	Gly	Lys	Thr	Gly					
				200					205					210					
Ile	Lys	Thr	Ser	Cys	Leu	Cys	Pro	Val	Phe	Val	Asn	Thr	Gly	Phe					
				215					220					225					
Thr	Lys	Asn	Pro	Ser	Thr	Arg	Leu	Trp	Pro	Val	Leu	Glu	Thr	Asp					
				230					235					240					
Glu	Val	Val	Arg	Ser	Leu	Ile	Asp	Gly	Ile	Leu	Thr	Asn	Lys	Lys					
				245					250					255					
Met	Ile	Phe	Val	Pro	Ser	Tyr	Ile	Asn	Ile	Phe	Leu	Arg	Leu	Gln					
				260					265					270					
Lys	Phe	Leu	Pro	Glu	Arg	Ala	Ser	Ala	Ile	Leu	Asn	Arg	Met	Gln					
				275					280					285					
Asn	Ile	Gln	Phe	Glu	Ala	Val	Val	Gly	His	Lys	Ile	Lys	Met	Lys					
				290					295					300					

<210> 465

<211> 1547

<212> DNA

<213> Homo sapiens

<400> 465

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cggcggcggc tgcgggcgcg aggtgagggg cgcgaggtga ggggcgcgag 50
gttcccagca ggatgccccg gctctgcagg aagctgaagt gagaggcccc 100
gagaggcccc agcccgcccc gggcaggatg accaaggccc ggctgttccg 150
gctgtggctg gtgctggggg cgggtgttcat gatcctgctg atcatcgtgt 200
actgggacag cgcaggcgcc gcgcacttct acttgcacac gtccttctct 250
aggccgcaca cggggccgcc gctgcccacg cccgggccgg acagggacag 300
ggagctcacg gccgactccg atgtcgacga gtttctggac aagtttctca 350
gtgctggcgt gaagcagagc gaccttccca gaaaggagac ggagcagccg 400
cctgcgccgg ggagcatgga ggagagcgtg agaggctacg actggtcccc 450
gcgcgacgcc cggcgcagcc cagaccaggg ccggcagcag gcggagcgga 500
ggagcgtgct gcggggcttc tgcgccaaact ccagcctggc cttccccacc 550

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aaggagcgcg cattcgacga catccccaac tcggagctga gccacctgat 600
cgtggacgac cggcacgggg ccatctactg ctacgtgccc aaggtggcct 650
gcaccaactg gaagcgcgctg atgatcgtgc tgagcggaag cctgctgcac 700
cgcggtgcmc cctaccgcmga cccgctgcmc atcccgcmcg agcacgtgca 750
caacgccagc gcgcacctga ccttcaacaa gttctggcmc cgctacggga 800
agctctcccg ccacctcatg aaggtaagc tcaagaagta caccaagttc 850
ctcttcgtgc ggcacccctt cgtgcmgctg atctccgctt tccgcagcaa 900
gttcgagctg gagaacgagg agttctaccg caagttcgcc gtgcccagtc 950
tgcmgctgta cgccaaccac accagcctgc ccgctcmggc gcgcgaggcc 1000
ttccgcmctg gcctcaaggt gtcttcgccc aacttcatcc agtacctgct 1050
ggaccmcmac acggagaagc tggcmgctt caacgagcac tggcmgcmgg 1100
tgtaccgctt ctgccacccg tgccagatcm actacgactt cgtggggag 1150
ctggagactc tggacgagga cmcmcmcmcm ctgctgcagc tactccaggt 1200
ggaccmcmcm ctccgcttcc ccccmcmcmta cmgmcmcmcm accmcmcmcm 1250
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ctgtataaac tctacgagga cmactttggt ctcttcgcmct acccmcmcm 1350
cmgaaacctc ctcmcmcmcm gaaagctttc gcmgttgctt ttctcmcmcm 1400
cctgmcmcmcm gacmcmcmcm cactcmcmgt tttttatgac ctacgatttt 1450
gcaatctggg cttcttgctt actcmcmcm ctctatccat tgagtactgt 1500
atcmgatattg ttttttaaga ttaatatatt tcaggtattt aatacmga 1547

```

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<210> 466
<211> 414
<212> PRT
<213> Homo sapiens

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<400> 466
Met Thr Lys Ala Arg Leu Phe Arg Leu Trp Leu Val Leu Gly Ser
 1             5             10            15

Val Phe Met Ile Leu Leu Ile Ile Val Tyr Trp Asp Ser Ala Gly
          20             25            30

Ala Ala His Phe Tyr Leu His Thr Ser Phe Ser Arg Pro His Thr
          35             40            45

Gly Pro Pro Leu Pro Thr Pro Gly Pro Asp Arg Asp Arg Glu Leu
          50             55            60

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Thr	Ala	Asp	Ser	Asp	Val	Asp	Glu	Phe	Leu	Asp	Lys	Phe	Leu	Ser	65	70	75
Ala	Gly	Val	Lys	Gln	Ser	Asp	Leu	Pro	Arg	Lys	Glu	Thr	Glu	Gln	80	85	90
Pro	Pro	Ala	Pro	Gly	Ser	Met	Glu	Glu	Ser	Val	Arg	Gly	Tyr	Asp	95	100	105
Trp	Ser	Pro	Arg	Asp	Ala	Arg	Arg	Ser	Pro	Asp	Gln	Gly	Arg	Gln	110	115	120
Gln	Ala	Glu	Arg	Arg	Ser	Val	Leu	Arg	Gly	Phe	Cys	Ala	Asn	Ser	125	130	135
Ser	Leu	Ala	Phe	Pro	Thr	Lys	Glu	Arg	Ala	Phe	Asp	Asp	Ile	Pro	140	145	150
Asn	Ser	Glu	Leu	Ser	His	Leu	Ile	Val	Asp	Asp	Arg	His	Gly	Ala	155	160	165
Ile	Tyr	Cys	Tyr	Val	Pro	Lys	Val	Ala	Cys	Thr	Asn	Trp	Lys	Arg	170	175	180
Val	Met	Ile	Val	Leu	Ser	Gly	Ser	Leu	Leu	His	Arg	Gly	Ala	Pro	185	190	195
Tyr	Arg	Asp	Pro	Leu	Arg	Ile	Pro	Arg	Glu	His	Val	His	Asn	Ala	200	205	210
Ser	Ala	His	Leu	Thr	Phe	Asn	Lys	Phe	Trp	Arg	Arg	Tyr	Gly	Lys	215	220	225
Leu	Ser	Arg	His	Leu	Met	Lys	Val	Lys	Leu	Lys	Lys	Tyr	Thr	Lys	230	235	240
Phe	Leu	Phe	Val	Arg	Asp	Pro	Phe	Val	Arg	Leu	Ile	Ser	Ala	Phe	245	250	255
Arg	Ser	Lys	Phe	Glu	Leu	Glu	Asn	Glu	Glu	Phe	Tyr	Arg	Lys	Phe	260	265	270
Ala	Val	Pro	Met	Leu	Arg	Leu	Tyr	Ala	Asn	His	Thr	Ser	Leu	Pro	275	280	285
Ala	Ser	Ala	Arg	Glu	Ala	Phe	Arg	Ala	Gly	Leu	Lys	Val	Ser	Phe	290	295	300
Ala	Asn	Phe	Ile	Gln	Tyr	Leu	Leu	Asp	Pro	His	Thr	Glu	Lys	Leu	305	310	315
Ala	Pro	Phe	Asn	Glu	His	Trp	Arg	Gln	Val	Tyr	Arg	Leu	Cys	His	320	325	330
Pro	Cys	Gln	Ile	Asp	Tyr	Asp	Phe	Val	Gly	Lys	Leu	Glu	Thr	Leu	335	340	345

Asp	Glu	Asp	Ala	Ala	Gln	Leu	Leu	Gln	Leu	Leu	Gln	Val	Asp	Arg	
				350					355					360	
Gln	Leu	Arg	Phe	Pro	Pro	Ser	Tyr	Arg	Asn	Arg	Thr	Ala	Ser	Ser	
				365					370					375	
Trp	Glu	Glu	Asp	Trp	Phe	Ala	Lys	Ile	Pro	Leu	Ala	Trp	Arg	Gln	
				380					385					390	
Gln	Leu	Tyr	Lys	Leu	Tyr	Glu	Ala	Asp	Phe	Val	Leu	Phe	Gly	Tyr	
				395					400					405	
Pro	Lys	Pro	Glu	Asn	Leu	Leu	Arg	Asp							
				410											

<210> 467

<211> 1071

<212> DNA

<213> Homo sapiens

<400> 467

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tcgggccaga attcggcacg aggcggcacg agggcgacgg cctcacgggg 50
ctttggaggt gaaagaggcc cagagtagag agagagagag accgacgtac 100
acgggatggc tacgggaacg cgctatgccg ggaagggtgt ggtcgtgacc 150
gggggcgggc gcggcatcgg agctgggatc gtgcgcgcct tcgtgaacag 200
cggggcccga gtggttatct gcgacaagga tgagtctggg ggccggggccc 250
tgagacagga gtcacctgga gctgtcttta tcctctgtga tgtgactcag 300
gaagatgatg tgaagaccct ggtttctgag accatccgcc gatttggccg 350
cctggattgt gttgtcaaca acgctggcca ccaccaccc ccacagaggc 400
ctgaggagac ctctgccag ggattccgcc agctgctgga gctgaaccta 450
ctggggacgt acaccttgac caagctcgcc ctcccctacc tgcggaagag 500
tcaagggaat gtcacaaaca tctccagcct ggtgggggca atcgccagg 550
cccaggcagt tccctatgtg gccaccaagg gggcagtaac agccatgacc 600
aaagctttgg ccctggatga aagtccatat ggtgtccgag tcaactgtat 650
ctccccagga aacatctgga ccccgtgtg ggaggagctg gcagccttaa 700
tgccagaccc tagggccaca atccgagagg gcatgctggc ccagccactg 750
ggccgcatgg gccagcccgc tgaggctggg gctgcggcag tgttcctggc 800
ctccgaagcc aacttctgca cgggcattga actgctcgtg acgggggggtg 850
cagagctggg gtacgggtgc aaggccagtc ggagcacccc cgtggacgcc 900

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cccgatatcc cttcctgatt tctctcattt ctacttgggg ccccttcct 950
aggactctcc caccctaaac tccaacctgt atcagatgca gcccctaacg 1000
ccttagactc taagcccagt tagcaaggtg ccgggtcacc ctgcaggttc 1050
ccataaaaaac gatttgcagc c 1071

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<210> 468
<211> 270
<212> PRT
<213> Homo sapiens

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<400> 468
Met Ala Thr Gly Thr Arg Tyr Ala Gly Lys Val Val Val Val Thr
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Gly Gly Gly Arg Gly Ile Gly Ala Gly Ile Val Arg Ala Phe Val
              20              25              30

Asn Ser Gly Ala Arg Val Val Ile Cys Asp Lys Asp Glu Ser Gly
              35              40              45

Gly Arg Ala Leu Glu Gln Glu Leu Pro Gly Ala Val Phe Ile Leu
              50              55              60

Cys Asp Val Thr Gln Glu Asp Asp Val Lys Thr Leu Val Ser Glu
              65              70              75

Thr Ile Arg Arg Phe Gly Arg Leu Asp Cys Val Val Asn Asn Ala
              80              85              90

Gly His His Pro Pro Pro Gln Arg Pro Glu Glu Thr Ser Ala Gln
              95              100             105

Gly Phe Arg Gln Leu Leu Glu Leu Asn Leu Leu Gly Thr Tyr Thr
              110             115             120

Leu Thr Lys Leu Ala Leu Pro Tyr Leu Arg Lys Ser Gln Gly Asn
              125             130             135

Val Ile Asn Ile Ser Ser Leu Val Gly Ala Ile Gly Gln Ala Gln
              140             145             150

Ala Val Pro Tyr Val Ala Thr Lys Gly Ala Val Thr Ala Met Thr
              155             160             165

Lys Ala Leu Ala Leu Asp Glu Ser Pro Tyr Gly Val Arg Val Asn
              170             175             180

Cys Ile Ser Pro Gly Asn Ile Trp Thr Pro Leu Trp Glu Glu Leu
              185             190             195

Ala Ala Leu Met Pro Asp Pro Arg Ala Thr Ile Arg Glu Gly Met
              200             205             210

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Leu	Ala	Gln	Pro	Leu	Gly	Arg	Met	Gly	Gln	Pro	Ala	Glu	Val	Gly
				215					220					225
Ala	Ala	Ala	Val	Phe	Leu	Ala	Ser	Glu	Ala	Asn	Phe	Cys	Thr	Gly
				230					235					240
Ile	Glu	Leu	Leu	Val	Thr	Gly	Gly	Ala	Glu	Leu	Gly	Tyr	Gly	Cys
				245					250					255
Lys	Ala	Ser	Arg	Ser	Thr	Pro	Val	Asp	Ala	Pro	Asp	Ile	Pro	Ser
				260					265					270

<210> 469  
 <211> 687  
 <212> DNA  
 <213> Homo sapiens

<400> 469  
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 cctcacaacc tgctgtttct tcttaccatt tccatcttcc tggggctggg 100  
 ccagcccagg agccccaaaa gcaagaggaa ggggcaaggg cggcctgggc 150  
 ccctggcccc tggccctcac caggtgccac tggacctggt gtcacggatg 200  
 aaaccgtatg cccgcatgga ggagtatgag aggaacatcg aggagatggt 250  
 ggcccagctg aggaacagct cagagctggc ccagagaaaag tgtgaggtca 300  
 acttgcagct gtggatgtcc aacaagagga gcctgtctcc ctggggctac 350  
 agcatcaacc acgaccccag ccgtatcccc gtggacctgc cggaggcacg 400  
 gtgcctgtgt ctgggctgtg tgaaccctt caccatgcag gaggaccgca 450  
 gcatggtgag cgtgccggtg ttcagccagg ttcctgtgcg ccgccgcctc 500  
 tgcccgccac cgccccgcac agggccttgc cgccagcgcg cagtcatgga 550  
 gaccatcgct gtgggctgca cctgcatctt ctgaatcacc tggcccagaa 600  
 gccaggccag cagcccgaga ccatactcct tgcacctttg tgccaagaaa 650  
 ggcctatgaa aagtaaacac tgacttttga aagcaag 687

<210> 470  
 <211> 180  
 <212> PRT  
 <213> Homo sapiens

<400> 470  
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 Phe Leu Gly Leu Gly Gln Pro Arg Ser Pro Lys Ser Lys Arg Lys  
 20 25 30



Gly	Gln	Gly	Arg	Pro	Gly	Pro	Leu	Ala	Pro	Gly	Pro	His	Gln	Val			
				35		.			40					45			
Pro	Leu	Asp	Leu	Val	Ser	Arg	Met	Lys	Pro	Tyr	Ala	Arg	Met	Glu			
				50					55					60			
Glu	Tyr	Glu	Arg	Asn	Ile	Glu	Glu	Met	Val	Ala	Gln	Leu	Arg	Asn			
				65					70					75			
Ser	Ser	Glu	Leu	Ala	Gln	Arg	Lys	Cys	Glu	Val	Asn	Leu	Gln	Leu			
				80					85					90			
Trp	Met	Ser	Asn	Lys	Arg	Ser	Leu	Ser	Pro	Trp	Gly	Tyr	Ser	Ile			
				95					100					105			
Asn	His	Asp	Pro	Ser	Arg	Ile	Pro	Val	Asp	Leu	Pro	Glu	Ala	Arg			
				110					115					120			
Cys	Leu	Cys	Leu	Gly	Cys	Val	Asn	Pro	Phe	Thr	Met	Gln	Glu	Asp			
				125					130					135			
Arg	Ser	Met	Val	Ser	Val	Pro	Val	Phe	Ser	Gln	Val	Pro	Val	Arg			
				140					145					150			
Arg	Arg	Leu	Cys	Pro	Pro	Pro	Pro	Arg	Thr	Gly	Pro	Cys	Arg	Gln			
				155					160					165			
Arg	Ala	Val	Met	Glu	Thr	Ile	Ala	Val	Gly	Cys	Thr	Cys	Ile	Phe			
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<210> 471  
 <211> 2368  
 <212> DNA  
 <213> Homo sapiens

<400> 471  
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 cggcccgag ctaacggcgc tctggccgc ctggatcgcg gctgtggcg 200  
 cgacggcagg ccccgaggag gccgcgctgc cgccggagca gagccgggtc 250  
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 gctgaaattt tacgccccat ggtgtccatc ctgccagcag actgattcag 350  
 aatgggaggc ttttgcaaag aatggtgaaa tacttcagat cagtgtgggg 400  
 aaggtagatg tcattcaaga accaggtttg agtggccgct tctttgtcac 450  
 cactctccca gcattttttc atgcaaagga tgggatattc cgccgttattc 500

gtggcccagg aatcttcgaa gacctgcaga attatatctt agagaagaaa 550  
tggcaatcag tcgagcctct gactggctgg aaatccccag cttctctaac 600  
gatgtctgga atggctggtc tttttagcat ctctggcaag atatggcatc 650  
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ctgagcgttc tgagcagaat cggagatcag aggaggctca tagagctgaa 850  
cagttgcagg atgcggagga ggaaaaagat gattcaaatg aagaagaaaa 900  
caaagacagc cttgtagatg atgaagaaga gaaagaagat cttggcgatg 950  
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gatgaggaga gaagtgaggc caatgatcag gggccccag gagaggacgg 1050  
tgtgaccggg gaggaagtag agcctgagga ggctgaagaa ggcattctctg 1100  
agcaaccctg cccagctgac acagaggtgg tggaagactc cttgaggcag 1150  
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caagaataca caccaaaaaca atatgtcagc ttccctttgg cctgcagttt 1250  
gtaccaaata cttaattttt cctgaatgag caagcttctc ttaaaagatg 1300  
ctctctagtc atttgggtctc atggcagtaa gcctcatgta tactaaggag 1350  
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gatctgtttg gagactggga tgggaacaag ttcatttact taggggtcag 1450  
agagtctcga ccagaggagg ccattcccag tctaatacag caccttccag 1500  
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taaccataac ccctgaagct gtgactgcc aacatctcaa atgaaatgtt 1950

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 aaggtagtct tgtgaagaaa agttgaatac tgTTTTgttt tcatctcaag 2150  
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 gattttcctt cagtgatgtg cttttggtga aagaattaat gaactccagt 2250  
 acctgaaagt gaaagatttg attttgtttc catcttctgt aatcttccaa 2300  
 agaattatat ctttgtaaat ctctcaatac tcaatctact gtaagtaccc 2350  
 aggaggcta atttcttt 2368

<210> 472  
 <211> 349  
 <212> PRT  
 <213> Homo sapiens

<400> 472  
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 20 25 30  
 Ala Leu Pro Pro Glu Gln Ser Arg Val Gln Pro Met Thr Ala Ser  
 35 40 45  
 Asn Trp Thr Leu Val Met Glu Gly Glu Trp Met Leu Lys Phe Tyr  
 50 55 60  
 Ala Pro Trp Cys Pro Ser Cys Gln Gln Thr Asp Ser Glu Trp Glu  
 65 70 75  
 Ala Phe Ala Lys Asn Gly Glu Ile Leu Gln Ile Ser Val Gly Lys  
 80 85 90  
 Val Asp Val Ile Gln Glu Pro Gly Leu Ser Gly Arg Phe Phe Val  
 95 100 105  
 Thr Thr Leu Pro Ala Phe Phe His Ala Lys Asp Gly Ile Phe Arg  
 110 115 120  
 Arg Tyr Arg Gly Pro Gly Ile Phe Glu Asp Leu Gln Asn Tyr Ile  
 125 130 135  
 Leu Glu Lys Lys Trp Gln Ser Val Glu Pro Leu Thr Gly Trp Lys  
 140 145 150  
 Ser Pro Ala Ser Leu Thr Met Ser Gly Met Ala Gly Leu Phe Ser  
 155 160 165

Ile Ser Gly Lys	Ile Trp His Leu His	Asn Tyr Phe Thr Val Thr
170	175	180
Leu Gly Ile Pro	Ala Trp Cys Ser Tyr	Val Phe Phe Val Ile Ala
185	190	195
Thr Leu Val Phe	Gly Leu Phe Met Gly	Leu Val Leu Val Val Ile
200	205	210
Ser Glu Cys Phe	Tyr Val Pro Leu Pro	Arg His Leu Ser Glu Arg
215	220	225
Ser Glu Gln Asn	Arg Arg Ser Glu Glu	Ala His Arg Ala Glu Gln
230	235	240
Leu Gln Asp Ala	Glu Glu Glu Lys Asp	Asp Ser Asn Glu Glu Glu
245	250	255
Asn Lys Asp Ser	Leu Val Asp Asp Glu	Glu Glu Lys Glu Asp Leu
260	265	270
Gly Asp Glu Asp	Glu Ala Glu Glu Glu	Glu Glu Glu Asp Asn Leu
275	280	285
Ala Ala Gly Val	Asp Glu Glu Arg Ser	Glu Ala Asn Asp Gln Gly
290	295	300
Pro Pro Gly Glu	Asp Gly Val Thr Arg	Glu Glu Val Glu Pro Glu
305	310	315
Glu Ala Glu Glu	Gly Ile Ser Glu Gln	Pro Cys Pro Ala Asp Thr
320	325	330
Glu Val Val Glu	Asp Ser Leu Arg Gln	Arg Lys Ser Gln His Ala
335	340	345

Asp Lys Gly Leu

<210> 473

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 473

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<210> 474

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 474

ctctcctcat ccacaccagc agcc 24

<210> 475

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 475

gtggatgctg aaattttacg ccccatgggtg tccatcctgc cagc 44

<210> 476

<211> 2478

<212> DNA

<213> Homo sapiens

<400> 476

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tcaagaacaa tggaatatca tcctgattta gaaaatttgg atgaagatgg 200  
atatactcaa ttacacttcg actctcaaag caataccagg atagctgttg 250  
tttcagagaa aggatcgtgt gctgcattct ctccttggcg cctcattgct 300  
gtaatttttg gaatcctatg cttggtaata ctggatgatg ctgtgggcct 350  
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acaggcgtga gccactgcac ccagcctaga atcttgata atatgtaatt 2000  
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tacataaaaa tacataaaat ctgatgatga atataaaaaa gtaaccaacc 2100  
tcattggaac aagtattaac attttggaat atgttttatt agttttgtga 2150  
tgtactgttt tacaattttt accatttttt tcagtaatta ctgtaaaatg 2200  
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2478

<210> 477  
 <211> 201  
 <212> PRT  
 <213> Homo sapiens

<400> 477  
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                   20                  25                  30  
 Val Ser Glu Lys Gly Ser Cys Ala Ala Ser Pro Pro Trp Arg Leu  
                   35                  40                  45  
 Ile Ala Val Ile Leu Gly Ile Leu Cys Leu Val Ile Leu Val Ile  
                   50                  55                  60  
 Ala Val Val Leu Gly Thr Met Gly Val Leu Ser Ser Pro Cys Pro  
                   65                  70                  75  
 Pro Asn Trp Ile Ile Tyr Glu Lys Ser Cys Tyr Leu Phe Ser Met  
                   80                  85                  90  
 Ser Leu Asn Ser Trp Asp Gly Ser Lys Arg Gln Cys Trp Gln Leu  
                   95                  100                  105  
 Gly Ser Asn Leu Leu Lys Ile Asp Ser Ser Asn Glu Leu Gly Phe  
                   110                  115                  120  
 Ile Val Lys Gln Val Ser Ser Gln Pro Asp Asn Ser Phe Trp Ile  
                   125                  130                  135  
 Gly Leu Ser Arg Pro Gln Thr Glu Val Pro Trp Leu Trp Glu Asp  
                   140                  145                  150  
 Gly Ser Thr Phe Ser Ser Asn Leu Phe Gln Ile Arg Thr Thr Ala  
                   155                  160                  165  
 Thr Gln Glu Asn Pro Ser Pro Asn Cys Val Trp Ile His Val Ser  
                   170                  175                  180  
 Val Ile Tyr Asp Gln Leu Cys Ser Val Pro Ser Tyr Ser Ile Cys  
                   185                  190                  195  
 Glu Lys Lys Phe Ser Met  
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<210> 478

<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

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<210> 479  
<211> 20  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 479  
acaagtgtct tcccaacctg 20

<210> 480  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 480  
atcctcccag agccatggta cctc 24

<210> 481  
<211> 51  
<212> DNA  
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<223> Synthetic oligonucleotide probe

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t 51

<210> 482  
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<212> DNA  
<213> Homo sapiens

<400> 482  
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tcttggtca tcgtaacctc cacctcccgg gttcaagtga ttctcatgcc 150



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<210> 483

<211> 693

<212> PRT

<213> Homo sapiens

<400> 483

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				20					25					30
Asp	Phe	Arg	Phe	Cys	Ser	Gln	Arg	Asn	Gln	Thr	His	Arg	Ser	Ser
				35					40					45
Leu	His	Tyr	Lys	Pro	Thr	Pro	Asp	Leu	Arg	Ile	Ser	Ile	Glu	Asn
				50					55					60
Ser	Glu	Glu	Ala	Leu	Thr	Val	His	Ala	Pro	Phe	Pro	Ala	Ala	His
				65					70					75
Pro	Ala	Ser	Arg	Ser	Phe	Pro	Asp	Pro	Arg	Gly	Leu	Tyr	His	Phe
				80					85					90

Cys	Leu	Tyr	Trp	Asn	Arg	His	Ala	Gly	Arg	Leu	His	Leu	Leu	Tyr	95	100	105
Gly	Lys	Arg	Asp	Phe	Leu	Leu	Ser	Asp	Lys	Ala	Ser	Ser	Leu	Leu	110	115	120
Cys	Phe	Gln	His	Gln	Glu	Glu	Ser	Leu	Ala	Gln	Gly	Pro	Pro	Leu	125	130	135
Leu	Ala	Thr	Ser	Val	Thr	Ser	Trp	Trp	Ser	Pro	Gln	Asn	Ile	Ser	140	145	150
Leu	Pro	Ser	Ala	Ala	Ser	Phe	Thr	Phe	Ser	Phe	His	Ser	Pro	Pro	155	160	165
His	Thr	Ala	Ala	His	Asn	Ala	Ser	Val	Asp	Met	Cys	Glu	Leu	Lys	170	175	180
Arg	Asp	Leu	Gln	Leu	Leu	Ser	Gln	Phe	Leu	Lys	His	Pro	Gln	Lys	185	190	195
Ala	Ser	Arg	Arg	Pro	Ser	Ala	Ala	Pro	Ala	Ser	Gln	Gln	Leu	Gln	200	205	210
Ser	Leu	Glu	Ser	Lys	Leu	Thr	Ser	Val	Arg	Phe	Met	Gly	Asp	Met	215	220	225
Val	Ser	Phe	Glu	Glu	Asp	Arg	Ile	Asn	Ala	Thr	Val	Trp	Lys	Leu	230	235	240
Gln	Pro	Thr	Ala	Gly	Leu	Gln	Asp	Leu	His	Ile	His	Ser	Arg	Gln	245	250	255
Glu	Glu	Glu	Gln	Ser	Glu	Ile	Met	Glu	Tyr	Ser	Val	Leu	Leu	Pro	260	265	270
Arg	Thr	Leu	Phe	Gln	Arg	Thr	Lys	Gly	Arg	Ser	Gly	Glu	Ala	Glu	275	280	285
Lys	Arg	Leu	Leu	Leu	Val	Asp	Phe	Ser	Ser	Gln	Ala	Leu	Phe	Gln	290	295	300
Asp	Lys	Asn	Ser	Ser	Gln	Val	Leu	Gly	Glu	Lys	Val	Leu	Gly	Ile	305	310	315
Val	Val	Gln	Asn	Thr	Lys	Val	Ala	Asn	Leu	Thr	Glu	Pro	Val	Val	320	325	330
Leu	Thr	Phe	Gln	His	Gln	Leu	Gln	Pro	Lys	Asn	Val	Thr	Leu	Gln	335	340	345
Cys	Val	Phe	Trp	Val	Glu	Asp	Pro	Thr	Leu	Ser	Ser	Pro	Gly	His	350	355	360
Trp	Ser	Ser	Ala	Gly	Cys	Glu	Thr	Val	Arg	Arg	Glu	Thr	Gln	Thr	365	370	375

Ser	Cys	Phe	Cys	Asn	His	Leu	Thr	Tyr	Phe	Ala	Val	Leu	Met	Val	
				380					385					390	
Ser	Ser	Val	Glu	Val	Asp	Ala	Val	His	Lys	His	Tyr	Leu	Ser	Leu	
				395					400					405	
Leu	Ser	Tyr	Val	Gly	Cys	Val	Val	Ser	Ala	Leu	Ala	Cys	Leu	Val	
				410					415					420	
Thr	Ile	Ala	Ala	Tyr	Leu	Cys	Ser	Arg	Val	Pro	Leu	Pro	Cys	Arg	
				425					430					435	
Arg	Lys	Pro	Arg	Asp	Tyr	Thr	Ile	Lys	Val	His	Met	Asn	Leu	Leu	
				440					445					450	
Leu	Ala	Val	Phe	Leu	Leu	Asp	Thr	Ser	Phe	Leu	Leu	Ser	Glu	Pro	
				455					460					465	
Val	Ala	Leu	Thr	Gly	Ser	Glu	Ala	Gly	Cys	Arg	Ala	Ser	Ala	Ile	
				470					475					480	
Phe	Leu	His	Phe	Ser	Leu	Leu	Thr	Cys	Leu	Ser	Trp	Met	Gly	Leu	
				485					490					495	
Glu	Gly	Tyr	Asn	Leu	Tyr	Arg	Leu	Val	Val	Glu	Val	Phe	Gly	Thr	
				500					505					510	
Tyr	Val	Pro	Gly	Tyr	Leu	Leu	Lys	Leu	Ser	Ala	Met	Gly	Trp	Gly	
				515					520					525	
Phe	Pro	Ile	Phe	Leu	Val	Thr	Leu	Val	Ala	Leu	Val	Asp	Val	Asp	
				530					535					540	
Asn	Tyr	Gly	Pro	Ile	Ile	Leu	Ala	Val	His	Arg	Thr	Pro	Glu	Gly	
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Val	Ile	Tyr	Pro	Ser	Met	Cys	Trp	Ile	Arg	Asp	Ser	Leu	Val	Ser	
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Tyr	Ile	Thr	Asn	Leu	Gly	Leu	Phe	Ser	Leu	Val	Phe	Leu	Phe	Asn	
				575					580					585	
Met	Ala	Met	Leu	Ala	Thr	Met	Val	Val	Gln	Ile	Leu	Arg	Leu	Arg	
				590					595					600	
Pro	His	Thr	Gln	Lys	Trp	Ser	His	Val	Leu	Thr	Leu	Leu	Gly	Leu	
				605					610					615	
Ser	Leu	Val	Leu	Gly	Leu	Pro	Trp	Ala	Leu	Ile	Phe	Phe	Ser	Phe	
				620					625					630	
Ala	Ser	Gly	Thr	Phe	Gln	Leu	Val	Val	Leu	Tyr	Leu	Phe	Ser	Ile	
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Ile	Thr	Ser	Phe	Gln	Gly	Phe	Leu	Ile	Phe	Ile	Trp	Tyr	Trp	Ser	
				650					655					660	

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Ser Asp Ser Ala Arg Leu Pro Ile Ser Ser Gly Ser Thr Ser Ser  
680 685 690

Ser Arg Ile

<210> 484  
<211> 516  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 68, 70, 84, 147  
<223> unknown base

<400> 484  
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ctgctgctgg ccgtcttctt gctggacacg agcttctctg tcagcgnagc 150  
cgggtggccct gacaggctct gaaggctggc tgccgagcca gtgccatctt 200  
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<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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tggaggccta gatgcggtg gacg 24

<210> 487

<211> 2849

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 2715

<223> unknown base

<400> 487

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<211> 345  
<212> PRT  
<213> Homo sapiens

<400> 488  
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20 25 30  
Gln Phe Ser Ser Asn Lys Glu Gln Asn Gly Val Gln Asp Pro Gln  
35 40 45  
His Glu Arg Ile Ile Thr Val Ser Thr Asn Gly Ser Ile His Ser  
50 55 60  
Pro Arg Phe Pro His Thr Tyr Pro Arg Asn Thr Val Leu Val Trp  
65 70 75  
Arg Leu Val Ala Val Glu Glu Asn Val Trp Ile Gln Leu Thr Phe  
80 85 90  
Asp Glu Arg Phe Gly Leu Glu Asp Pro Glu Asp Asp Ile Cys Lys  
95 100 105  
Tyr Asp Phe Val Glu Val Glu Glu Pro Ser Asp Gly Thr Ile Leu  
110 115 120  
Gly Arg Trp Cys Gly Ser Gly Thr Val Pro Gly Lys Gln Ile Ser  
125 130 135  
Lys Gly Asn Gln Ile Arg Ile Arg Phe Val Ser Asp Glu Tyr Phe  
140 145 150  
Pro Ser Glu Pro Gly Phe Cys Ile His Tyr Asn Ile Val Met Pro  
155 160 165

Gln Phe Thr Glu	Ala Val Ser Pro Ser	Val Leu Pro Pro Ser	Ala
	170	175	180
Leu Pro Leu Asp	Leu Leu Asn Asn Ala	Ile Thr Ala Phe Ser	Thr
	185	190	195
Leu Glu Asp Leu	Ile Arg Tyr Leu Glu	Pro Glu Arg Trp Gln	Leu
	200	205	210
Asp Leu Glu Asp	Leu Tyr Arg Pro Thr	Trp Gln Leu Leu Gly	Lys
	215	220	225
Ala Phe Val Phe	Gly Arg Lys Ser Arg	Val Val Asp Leu Asn	Leu
	230	235	240
Leu Thr Glu Glu	Val Arg Leu Tyr Ser	Cys Thr Pro Arg Asn	Phe
	245	250	255
Ser Val Ser Ile	Arg Glu Glu Leu Lys	Arg Thr Asp Thr Ile	Phe
	260	265	270
Trp Pro Gly Cys	Leu Leu Val Lys Arg	Cys Gly Gly Asn Cys	Ala
	275	280	285
Cys Cys Leu His	Asn Cys Asn Glu Cys	Gln Cys Val Pro Ser	Lys
	290	295	300
Val Thr Lys Lys	Tyr His Glu Val Leu	Gln Leu Arg Pro Lys	Thr
	305	310	315
Gly Val Arg Gly	Leu His Lys Ser Leu	Thr Asp Val Ala Leu	Glu
	320	325	330
His His Glu Glu	Cys Asp Cys Val Cys	Arg Gly Ser Thr Gly	Gly
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<210> 489

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 489

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<210> 490

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 490

gaactaaaga gaaccgatac cattttctgg ccaggttgtc 40

<210> 491

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 491

caccacagcg tttaaccagg 20

<210> 492

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 492

acaacaggca cagttccac 20

<210> 493

<211> 21

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 493

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<210> 494

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<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 494

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<210> 495

<211> 3283

<212> DNA

<213> Homo sapiens

<400> 495

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ggacactgaa gagacaaatt cttatccttt ttaacataat cctaatttcc 150

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<210> 496  
 <211> 1049  
 <212> PRT  
 <213> Homo sapiens

<400> 496  
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 20 25 30  
 Pro Lys Thr Leu Pro Cys Asp Val Thr Leu Asp Val Pro Lys Asn  
 35 40 45  
 His Val Ile Val Asp Cys Thr Asp Lys His Leu Thr Glu Ile Pro  
 50 55 60  
 Gly Gly Ile Pro Thr Asn Thr Thr Asn Leu Thr Leu Thr Ile Asn  
 65 70 75  
 His Ile Pro Asp Ile Ser Pro Ala Ser Phe His Arg Leu Asp His  
 80 85 90  
 Leu Val Glu Ile Asp Phe Arg Cys Asn Cys Val Pro Ile Pro Leu  
 95 100 105  
 Gly Ser Lys Asn Asn Met Cys Ile Lys Arg Leu Gln Ile Lys Pro  
 110 115 120  
 Arg Ser Phe Ser Gly Leu Thr Tyr Leu Lys Ser Leu Tyr Leu Asp  
 125 130 135  
 Gly Asn Gln Leu Leu Glu Ile Pro Gln Gly Leu Pro Pro Ser Leu  
 140 145 150  
 Gln Leu Leu Ser Leu Glu Ala Asn Asn Ile Phe Ser Ile Arg Lys  
 155 160 165  
 Glu Asn Leu Thr Glu Leu Ala Asn Ile Glu Ile Leu Tyr Leu Gly  
 170 175 180  
 Gln Asn Cys Tyr Tyr Arg Asn Pro Cys Tyr Val Ser Tyr Ser Ile  
 185 190 195

Glu Lys Asp Ala	Phe Leu Asn Leu Thr	Lys Leu Lys Val Leu	Ser
	200	205	210
Leu Lys Asp Asn	Asn Val Thr Ala Val	Pro Thr Val Leu Pro	Ser
	215	220	225
Thr Leu Thr Glu	Leu Tyr Leu Tyr Asn	Asn Met Ile Ala Lys	Ile
	230	235	240
Gln Glu Asp Asp	Phe Asn Asn Leu Asn	Gln Leu Gln Ile Leu	Asp
	245	250	255
Leu Ser Gly Asn	Cys Pro Arg Cys Tyr	Asn Ala Pro Phe Pro	Cys
	260	265	270
Ala Pro Cys Lys	Asn Asn Ser Pro Leu	Gln Ile Pro Val Asn	Ala
	275	280	285
Phe Asp Ala Leu	Thr Glu Leu Lys Val	Leu Arg Leu His Ser	Asn
	290	295	300
Ser Leu Gln His	Val Pro Pro Arg Trp	Phe Lys Asn Ile Asn	Lys
	305	310	315
Leu Gln Glu Leu	Asp Leu Ser Gln Asn	Phe Leu Ala Lys Glu	Ile
	320	325	330
Gly Asp Ala Lys	Phe Leu His Phe Leu	Pro Ser Leu Ile Gln	Leu
	335	340	345
Asp Leu Ser Phe	Asn Phe Glu Leu Gln	Val Tyr Arg Ala Ser	Met
	350	355	360
Asn Leu Ser Gln	Ala Phe Ser Ser Leu	Lys Ser Leu Lys Ile	Leu
	365	370	375
Arg Ile Arg Gly	Tyr Val Phe Lys Glu	Leu Lys Ser Phe Asn	Leu
	380	385	390
Ser Pro Leu His	Asn Leu Gln Asn Leu	Glu Val Leu Asp Leu	Gly
	395	400	405
Thr Asn Phe Ile	Lys Ile Ala Asn Leu	Ser Met Phe Lys Gln	Phe
	410	415	420
Lys Arg Leu Lys	Val Ile Asp Leu Ser	Val Asn Lys Ile Ser	Pro
	425	430	435
Ser Gly Asp Ser	Ser Glu Val Gly Phe	Cys Ser Asn Ala Arg	Thr
	440	445	450
Ser Val Glu Ser	Tyr Glu Pro Gln Val	Leu Glu Gln Leu His	Tyr
	455	460	465
Phe Arg Tyr Asp	Lys Tyr Ala Arg Ser	Cys Arg Phe Lys Asn	Lys
	470	475	480

Glu	Ala	Ser	Phe	Met	Ser	Val	Asn	Glu	Ser	Cys	Tyr	Lys	Tyr	Gly	485	490	495
Gln	Thr	Leu	Asp	Leu	Ser	Lys	Asn	Ser	Ile	Phe	Phe	Val	Lys	Ser	500	505	510
Ser	Asp	Phe	Gln	His	Leu	Ser	Phe	Leu	Lys	Cys	Leu	Asn	Leu	Ser	515	520	525
Gly	Asn	Leu	Ile	Ser	Gln	Thr	Leu	Asn	Gly	Ser	Glu	Phe	Gln	Pro	530	535	540
Leu	Ala	Glu	Leu	Arg	Tyr	Leu	Asp	Phe	Ser	Asn	Asn	Arg	Leu	Asp	545	550	555
Leu	Leu	His	Ser	Thr	Ala	Phe	Glu	Glu	Leu	His	Lys	Leu	Glu	Val	560	565	570
Leu	Asp	Ile	Ser	Ser	Asn	Ser	His	Tyr	Phe	Gln	Ser	Glu	Gly	Ile	575	580	585
Thr	His	Met	Leu	Asn	Phe	Thr	Lys	Asn	Leu	Lys	Val	Leu	Gln	Lys	590	595	600
Leu	Met	Met	Asn	Asp	Asn	Asp	Ile	Ser	Ser	Ser	Thr	Ser	Arg	Thr	605	610	615
Met	Glu	Ser	Glu	Ser	Leu	Arg	Thr	Leu	Glu	Phe	Arg	Gly	Asn	His	620	625	630
Leu	Asp	Val	Leu	Trp	Arg	Glu	Gly	Asp	Asn	Arg	Tyr	Leu	Gln	Leu	635	640	645
Phe	Lys	Asn	Leu	Leu	Lys	Leu	Glu	Glu	Leu	Asp	Ile	Ser	Lys	Asn	650	655	660
Ser	Leu	Ser	Phe	Leu	Pro	Ser	Gly	Val	Phe	Asp	Gly	Met	Pro	Pro	665	670	675
Asn	Leu	Lys	Asn	Leu	Ser	Leu	Ala	Lys	Asn	Gly	Leu	Lys	Ser	Phe	680	685	690
Ser	Trp	Lys	Lys	Leu	Gln	Cys	Leu	Lys	Asn	Leu	Glu	Thr	Leu	Asp	695	700	705
Leu	Ser	His	Asn	Gln	Leu	Thr	Thr	Val	Pro	Glu	Arg	Leu	Ser	Asn	710	715	720
Cys	Ser	Arg	Ser	Leu	Lys	Asn	Leu	Ile	Leu	Lys	Asn	Asn	Gln	Ile	725	730	735
Arg	Ser	Leu	Thr	Lys	Tyr	Phe	Leu	Gln	Asp	Ala	Phe	Gln	Leu	Arg	740	745	750
Tyr	Leu	Asp	Leu	Ser	Ser	Asn	Lys	Ile	Gln	Met	Ile	Gln	Lys	Thr	755	760	765



Ser	Phe	Pro	Glu	Asn	Val	Leu	Asn	Asn	Leu	Lys	Met	Leu	Leu	Leu	
				770					775					780	
His	His	Asn	Arg	Phe	Leu	Cys	Thr	Cys	Asp	Ala	Val	Trp	Phe	Val	
				785					790					795	
Trp	Trp	Val	Asn	His	Thr	Glu	Val	Thr	Ile	Pro	Tyr	Leu	Ala	Thr	
				800					805					810	
Asp	Val	Thr	Cys	Val	Gly	Pro	Gly	Ala	His	Lys	Gly	Gln	Ser	Val	
				815					820					825	
Ile	Ser	Leu	Asp	Leu	Tyr	Thr	Cys	Glu	Leu	Asp	Leu	Thr	Asn	Leu	
				830					835					840	
Ile	Leu	Phe	Ser	Leu	Ser	Ile	Ser	Val	Ser	Leu	Phe	Leu	Met	Val	
				845					850					855	
Met	Met	Thr	Ala	Ser	His	Leu	Tyr	Phe	Trp	Asp	Val	Trp	Tyr	Ile	
				860					865					870	
Tyr	His	Phe	Cys	Lys	Ala	Lys	Ile	Lys	Gly	Tyr	Gln	Arg	Leu	Ile	
				875					880					885	
Ser	Pro	Asp	Cys	Cys	Tyr	Asp	Ala	Phe	Ile	Val	Tyr	Asp	Thr	Lys	
				890					895					900	
Asp	Pro	Ala	Val	Thr	Glu	Trp	Val	Leu	Ala	Glu	Leu	Val	Ala	Lys	
				905					910					915	
Leu	Glu	Asp	Pro	Arg	Glu	Lys	His	Phe	Asn	Leu	Cys	Leu	Glu	Glu	
				920					925					930	
Arg	Asp	Trp	Leu	Pro	Gly	Gln	Pro	Val	Leu	Glu	Asn	Leu	Ser	Gln	
				935					940					945	
Ser	Ile	Gln	Leu	Ser	Lys	Lys	Thr	Val	Phe	Val	Met	Thr	Asp	Lys	
				950					955					960	
Tyr	Ala	Lys	Thr	Glu	Asn	Phe	Lys	Ile	Ala	Phe	Tyr	Leu	Ser	His	
				965					970					975	
Gln	Arg	Leu	Met	Asp	Glu	Lys	Val	Asp	Val	Ile	Ile	Leu	Ile	Phe	
				980					985					990	
Leu	Glu	Lys	Pro	Phe	Gln	Lys	Ser	Lys	Phe	Leu	Gln	Leu	Arg	Lys	
				995					1000					1005	
Arg	Leu	Cys	Gly	Ser	Ser	Val	Leu	Glu	Trp	Pro	Thr	Asn	Pro	Gln	
				1010					1015					1020	
Ala	His	Pro	Tyr	Phe	Trp	Gln	Cys	Leu	Lys	Asn	Ala	Leu	Ala	Thr	
				1025					1030					1035	
Asp	Asn	His	Val	Ala	Tyr	Ser	Gln	Val	Phe	Lys	Glu	Thr	Val		
				1040					1045						

<210> 497  
<211> 4199  
<212> DNA  
<213> Homo sapiens

<400> 497  
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cctgctaata tctggttcct gtgagttatg cgccgaagaa aatttttcta 150  
gaagctatcc ttgtgatgag aaaaagcaaa atgactcagt tattgcagag 200  
tgcagcaatc gtcgactaca ggaagttccc caaacggtgg gcaaatatgt 250  
gacagaacta gacctgtctg ataatttcat cacacacata acgaatgaat 300  
catttcaagg gctgcaaaat ctactaaaa taaatctaaa ccacaacccc 350  
aatgtacagc accagaacgg aaatcccggg atacaatcaa atggcttgaa 400  
tatcacagac ggggcattcc tcaacctaaa aaacctagg gagttactgc 450  
ttgaagacaa ccagttaccc caaataccct ctggtttgcc agagtctttg 500  
acagaactta gtctaattca aaacaatata tacaacataa ctaaagaggg 550  
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<210> 498

<211> 1041

<212> PRT

<213> Homo sapiens

<400> 498

Met	Glu	Asn	Met	Phe	Leu	Gln	Ser	Ser	Met	Leu	Thr	Cys	Ile	Phe
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Leu	Leu	Ile	Ser	Gly	Ser	Cys	Glu	Leu	Cys	Ala	Glu	Glu	Asn	Phe
				20					25					30

Ser	Arg	Ser	Tyr	Pro	Cys	Asp	Glu	Lys	Lys	Gln	Asn	Asp	Ser	Val
				35					40					45

Ile	Ala	Glu	Cys	Ser	Asn	Arg	Arg	Leu	Gln	Glu	Val	Pro	Gln	Thr
				50					55					60

Val	Gly	Lys	Tyr	Val	Thr	Glu	Leu	Asp	Leu	Ser	Asp	Asn	Phe	Ile
				65					70					75

Thr	His	Ile	Thr	Asn	Glu	Ser	Phe	Gln	Gly	Leu	Gln	Asn	Leu	Thr
				80					85					90

Lys	Ile	Asn	Leu	Asn	His	Asn	Pro	Asn	Val	Gln	His	Gln	Asn	Gly
				95					100					105

Asn	Pro	Gly	Ile	Gln	Ser	Asn	Gly	Leu	Asn	Ile	Thr	Asp	Gly	Ala
				110					115					120

Phe	Leu	Asn	Leu	Lys	Asn	Leu	Arg	Glu	Leu	Leu	Leu	Glu	Asp	Asn
				125					130					135

Gln	Leu	Pro	Gln	Ile	Pro	Ser	Gly	Leu	Pro	Glu	Ser	Leu	Thr	Glu
				140					145					150

Leu	Ser	Leu	Ile	Gln	Asn	Asn	Ile	Tyr	Asn	Ile	Thr	Lys	Glu	Gly
				155					160					165

Ile	Ser	Arg	Leu	Ile	Asn	Leu	Lys	Asn	Leu	Tyr	Leu	Ala	Trp	Asn
				170					175					180

Cys	Tyr	Phe	Asn	Lys	Val	Cys	Glu	Lys	Thr	Asn	Ile	Glu	Asp	Gly
				185					190					195

Val	Phe	Glu	Thr	Leu	Thr	Asn	Leu	Glu	Leu	Leu	Ser	Leu	Ser	Phe
				200					205					210

Asn	Ser	Leu	Ser	His	Val	Pro	Pro	Lys	Leu	Pro	Ser	Ser	Leu	Arg
				215					220					225

Lys	Leu	Phe	Leu	Ser	Asn	Thr	Gln	Ile	Lys	Tyr	Ile	Ser	Glu	Glu
				230					235					240

Asp Phe Lys Gly	Leu Ile Asn Leu Thr	Leu Leu Asp Leu Ser Gly
245	250	255
Asn Cys Pro Arg	Cys Phe Asn Ala Pro	Phe Pro Cys Val Pro Cys
260	265	270
Asp Gly Gly Ala	Ser Ile Asn Ile Asp	Arg Phe Ala Phe Gln Asn
275	280	285
Leu Thr Gln Leu	Arg Tyr Leu Asn Leu	Ser Ser Thr Ser Leu Arg
290	295	300
Lys Ile Asn Ala	Ala Trp Phe Lys Asn	Met Pro His Leu Lys Val
305	310	315
Leu Asp Leu Glu	Phe Asn Tyr Leu Val	Gly Glu Ile Val Ser Gly
320	325	330
Ala Phe Leu Thr	Met Leu Pro Arg Leu	Glu Ile Leu Asp Leu Ser
335	340	345
Phe Asn Tyr Ile	Lys Gly Ser Tyr Pro	Gln His Ile Asn Ile Ser
350	355	360
Arg Asn Phe Ser	Lys Leu Leu Ser Leu	Arg Ala Leu His Leu Arg
365	370	375
Gly Tyr Val Phe	Gln Glu Leu Arg Glu	Asp Asp Phe Gln Pro Leu
380	385	390
Met Gln Leu Pro	Asn Leu Ser Thr Ile	Asn Leu Gly Ile Asn Phe
395	400	405
Ile Lys Gln Ile	Asp Phe Lys Leu Phe	Gln Asn Phe Ser Asn Leu
410	415	420
Glu Ile Ile Tyr	Leu Ser Glu Asn Arg	Ile Ser Pro Leu Val Lys
425	430	435
Asp Thr Arg Gln	Ser Tyr Ala Asn Ser	Ser Ser Phe Gln Arg His
440	445	450
Ile Arg Lys Arg	Arg Ser Thr Asp Phe	Glu Phe Asp Pro His Ser
455	460	465
Asn Phe Tyr His	Phe Thr Arg Pro Leu	Ile Lys Pro Gln Cys Ala
470	475	480
Ala Tyr Gly Lys	Ala Leu Asp Leu Ser	Leu Asn Ser Ile Phe Phe
485	490	495
Ile Gly Pro Asn	Gln Phe Glu Asn Leu	Pro Asp Ile Ala Cys Leu
500	505	510
Asn Leu Ser Ala	Asn Ser Asn Ala Gln	Val Leu Ser Gly Thr Glu
515	520	525

Phe Ser Ala Ile	Pro His Val Lys Tyr	Leu Asp Leu Thr Asn Asn	530	535	540
Arg Leu Asp Phe	Asp Asn Ala Ser Ala	Leu Thr Glu Leu Ser Asp	545	550	555
Leu Glu Val Leu	Asp Leu Ser Tyr Asn	Ser His Tyr Phe Arg Ile	560	565	570
Ala Gly Val Thr	His His Leu Glu Phe	Ile Gln Asn Phe Thr Asn	575	580	585
Leu Lys Val Leu	Asn Leu Ser His Asn	Asn Ile Tyr Thr Leu Thr	590	595	600
Asp Lys Tyr Asn	Leu Glu Ser Lys Ser	Leu Val Glu Leu Val Phe	605	610	615
Ser Gly Asn Arg	Leu Asp Ile Leu Trp	Asn Asp Asp Asp Asn Arg	620	625	630
Tyr Ile Ser Ile	Phe Lys Gly Leu Lys	Asn Leu Thr Arg Leu Asp	635	640	645
Leu Ser Leu Asn	Arg Leu Lys His Ile	Pro Asn Glu Ala Phe Leu	650	655	660
Asn Leu Pro Ala	Ser Leu Thr Glu Leu	His Ile Asn Asp Asn Met	665	670	675
Leu Lys Phe Phe	Asn Trp Thr Leu Leu	Gln Gln Phe Pro Arg Leu	680	685	690
Glu Leu Leu Asp	Leu Arg Gly Asn Lys	Leu Leu Phe Leu Thr Asp	695	700	705
Ser Leu Ser Asp	Phe Thr Ser Ser Leu	Arg Thr Leu Leu Leu Ser	710	715	720
His Asn Arg Ile	Ser His Leu Pro Ser	Gly Phe Leu Ser Glu Val	725	730	735
Ser Ser Leu Lys	His Leu Asp Leu Ser	Ser Asn Leu Leu Lys Thr	740	745	750
Ile Asn Lys Ser	Ala Leu Glu Thr Lys	Thr Thr Thr Lys Leu Ser	755	760	765
Met Leu Glu Leu	His Gly Asn Pro Phe	Glu Cys Thr Cys Asp Ile	770	775	780
Gly Asp Phe Arg	Arg Trp Met Asp Glu	His Leu Asn Val Lys Ile	785	790	795
Pro Arg Leu Val	Asp Val Ile Cys Ala	Ser Pro Gly Asp Gln Arg	800	805	810

Gly	Lys	Ser	Ile	Val	Ser	Leu	Glu	Leu	Thr	Thr	Cys	Val	Ser	Asp	815	820	825
Val	Thr	Ala	Val	Ile	Leu	Phe	Phe	Phe	Thr	Phe	Phe	Ile	Thr	Thr	830	835	840
Met	Val	Met	Leu	Ala	Ala	Leu	Ala	His	His	Leu	Phe	Tyr	Trp	Asp	845	850	855
Val	Trp	Phe	Ile	Tyr	Asn	Val	Cys	Leu	Ala	Lys	Val	Lys	Gly	Tyr	860	865	870
Arg	Ser	Leu	Ser	Thr	Ser	Gln	Thr	Phe	Tyr	Asp	Ala	Tyr	Ile	Ser	875	880	885
Tyr	Asp	Thr	Lys	Asp	Ala	Ser	Val	Thr	Asp	Trp	Val	Ile	Asn	Glu	890	895	900
Leu	Arg	Tyr	His	Leu	Glu	Glu	Ser	Arg	Asp	Lys	Asn	Val	Leu	Leu	905	910	915
Cys	Leu	Glu	Glu	Arg	Asp	Trp	Asp	Pro	Gly	Leu	Ala	Ile	Ile	Asp	920	925	930
Asn	Leu	Met	Gln	Ser	Ile	Asn	Gln	Ser	Lys	Lys	Thr	Val	Phe	Val	935	940	945
Leu	Thr	Lys	Lys	Tyr	Ala	Lys	Ser	Trp	Asn	Phe	Lys	Thr	Ala	Phe	950	955	960
Tyr	Leu	Ala	Leu	Gln	Arg	Leu	Met	Asp	Glu	Asn	Met	Asp	Val	Ile	965	970	975
Ile	Phe	Ile	Leu	Leu	Glu	Pro	Val	Leu	Gln	His	Ser	Gln	Tyr	Leu	980	985	990
Arg	Leu	Arg	Gln	Arg	Ile	Cys	Lys	Ser	Ser	Ile	Leu	Gln	Trp	Pro	995	1000	1005
Asp	Asn	Pro	Lys	Ala	Glu	Gly	Leu	Phe	Trp	Gln	Thr	Leu	Arg	Asn	1010	1015	1020
Val	Val	Leu	Thr	Glu	Asn	Asp	Ser	Arg	Tyr	Asn	Asn	Met	Tyr	Val	1025	1030	1035
Asp	Ser	Ile	Lys	Gln	Tyr										1040		

<210> 499

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe



<400> 499  
taaagaccca gctgtgaccg 20

<210> 500  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 500  
atccatgagc ctctgatggg 20

<210> 501  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 501  
atttatgtct cgaggaaagg gactggttac cagggcagcc agttc 45

<210> 502  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 502  
gccgagacaa aaacgttctc c 21

<210> 503  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 503  
catccatggt ctcattcatt agcc 24

<210> 504  
<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 504  
tcgacaacct catgcagagc atcaaccaa gcaagaaaac agtatt 46

<210> 505  
<211> 1738  
<212> DNA  
<213> Homo sapiens

<400> 505  
ccaggtccaa ctgcacctcg gttctatcga ttgaattccc cggggatcct 50  
ctagagatcc ctgcacctcg acccacgcgt ccgccaagct ggccctgcac 100  
ggctgcaagg gaggctcctg tggacaggcc aggacaggtg gcctcaggag 150  
gtgcctccag gcggccagtg ggctgaggc cccagcaagg gctaggggcc 200  
atctccagtc ccaggacaca gcagcggcca ccatggccac gcctgggctc 250  
cagcagcatc agcagcccc aggaccggg aggacaggt ggccccacc 300  
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cgccaggcca cccagaggag aaggccacc cgcctggagg cacaggccat 400  
gaggggctct caggaggtgc tgctgatgtg gcttctgggtg ttggcagtgg 450  
gcggcacaga gcacgcctac cggcccggcc gtaggggtgtg tgctgtccgg 500  
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tccagcctgg ccgctgccgc tgccctgcag gatggcgggg tgacacttgc 800  
cagtcagatg tggatgaatg cagtgtcagg aggggcggct gtccccagcg 850  
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agaagccacc tcggggtgac tgagcggaag gccaggcagg gccttcctcc 1350  
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gctgggtggg gcctcagtgg gggctgctgc ctgaccccca gcacaataaa 1600  
aatgaaacgt gaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1650  
aaagggcggc cgcgactcta gagtcgacct gcagaagctt ggccgcatg 1700  
gcccaacttg ttattgcag cttataatgg ttacaaat 1738

<210> 506  
<211> 273  
<212> PRT  
<213> Homo sapiens

<400> 506  
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20 25 30  
Cys Ala Val Arg Ala His Gly Asp Pro Val Ser Glu Ser Phe Val  
35 40 45  
Gln Arg Val Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg  
50 55 60  
Ala Cys Ser Thr Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg  
65 70 75  
Ser Pro Gly Leu Ala Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro  
80 85 90  
Gly Trp Lys Arg Thr Ser Gly Leu Pro Gly Ala Cys Gly Ala Ala  
95 100 105  
Ile Cys Gln Pro Pro Cys Arg Asn Gly Gly Ser Cys Val Gln Pro  
110 115 120  
Gly Arg Cys Arg Cys Pro Ala Gly Trp Arg Gly Asp Thr Cys Gln  
125 130 135  
Ser Asp Val Asp Glu Cys Ser Ala Arg Arg Gly Gly Cys Pro Gln  
140 145 150  
Arg Cys Ile Asn Thr Ala Gly Ser Tyr Trp Cys Gln Cys Trp Glu

	155		160		165
Gly His Ser Leu	Ser Ala Asp Gly Thr	Leu Cys Val Pro Lys	Gly		
	170		175		180
Gly Pro Pro Arg	Val Ala Pro Asn Pro	Thr Gly Val Asp Ser	Ala		
	185		190		195
Met Lys Glu Glu	Val Gln Arg Leu Gln	Ser Arg Val Asp Leu	Leu		
	200		205		210
Glu Glu Lys Leu	Gln Leu Val Leu Ala	Pro Leu His Ser Leu	Ala		
	215		220		225
Ser Gln Ala Leu	Glu His Gly Leu Pro	Asp Pro Gly Ser Leu	Leu		
	230		235		240
Val His Ser Phe	Gln Gln Leu Gly Arg	Ile Asp Ser Leu Ser	Glu		
	245		250		255
Gln Ile Ser Phe	Leu Glu Glu Gln Leu	Gly Ser Cys Ser Cys	Lys		
	260		265		270
Lys Asp Ser					

<210> 507  
 <211> 1700  
 <212> DNA  
 <213> Homo sapiens

<400> 507  
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 ccaccatggc cagcctggg ctccagcagc atcagagcag cccctgtggt 150  
 tggcagcaaa gttcagcttg gctgggcccg ctgtgagggg cttcgcgcta 200  
 cgccctgcgg tgtcccaggg gctgaggtct cctcatcttc tccctagcag 250  
 tggatgagca acccaacggg ggcccgggga ggggaactgg ccccagggga 300  
 gaggaacccc aaagccacat ctgtagccag gatgagcagt gtgaatccag 350  
 gcagcccca ggaccgggga ggcacaggtg gccccacca cccggaggag 400  
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 ccagaggaga aggccacccc gcctggaggc acaggccatg aggggctctc 500  
 aggaggtgct gctgatgtgg cttctgggtg tggcagtggg cggcacagag 550  
 cacgcctacc ggcccggccg tagggtgtgt gctgtccggg ctcacgggga 600  
 ccctgtctcc gagtcgttcg tgcagcgtgt gtaccagccc ttcctcacca 650

cctgcgacgg gcaccgggcc tgcagcacct accgaaccat ctataggacc 700  
gcctaccgcc gcagccctgg gctggcccct gccaggcctc gctacgcgtg 750  
ctgccccggc tggaagagga ccagcgggct tcctggggcc tgtggagcag 800  
caatatgcca gccgccatgc cggaacggag ggagctgtgt ccagcctggc 850  
cgctgccgct gccctgcagg atggcggggt gacacttgcc agtcagatgt 900  
ggatgaatgc agtgctagga ggggcggctg tcccagcgc tgcataca 950  
ccgccggcag ttactggtgc cagtgttggg aggggcacag cctgtctgca 1000  
gacggtacac tctgtgtgcc caagggaggg cccccaggg tggcccccaa 1050  
cccgaacagga gtggacagtgc caatgaagga agaagtgcag aggctgcagt 1100  
ccaggggtgga cctgctggag gagaagctgc agctgggtgct ggccccactg 1150  
cacagcctgg cctcgcaggc actggagcat gggctcccg accccggcag 1200  
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tcccaaggcc aggtggacct tcagctgagg gaaggtacga gctccctgct 1600  
ggagcctggg acccatggca caggccaggc agcccggagg ctgggtgggg 1650  
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<210> 508

<211> 273

<212> PRT

<213> Homo sapiens

<400> 508

Met	Arg	Gly	Ser	Gln	Glu	Val	Leu	Leu	Met	Trp	Leu	Leu	Val	Leu
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Ala	Val	Gly	Gly	Thr	Glu	His	Ala	Tyr	Arg	Pro	Gly	Arg	Arg	Val
				20					25					30

Cys	Ala	Val	Arg	Ala	His	Gly	Asp	Pro	Val	Ser	Glu	Ser	Phe	Val
				35					40					45

Gln	Arg	Val	Tyr	Gln	Pro	Phe	Leu	Thr	Thr	Cys	Asp	Gly	His	Arg	
				50					55					60	
Ala	Cys	Ser	Thr	Tyr	Arg	Thr	Ile	Tyr	Arg	Thr	Ala	Tyr	Arg	Arg	
				65					70					75	
Ser	Pro	Gly	Leu	Ala	Pro	Ala	Arg	Pro	Arg	Tyr	Ala	Cys	Cys	Pro	
				80					85					90	
Gly	Trp	Lys	Arg	Thr	Ser	Gly	Leu	Pro	Gly	Ala	Cys	Gly	Ala	Ala	
				95					100					105	
Ile	Cys	Gln	Pro	Pro	Cys	Arg	Asn	Gly	Gly	Ser	Cys	Val	Gln	Pro	
				110					115					120	
Gly	Arg	Cys	Arg	Cys	Pro	Ala	Gly	Trp	Arg	Gly	Asp	Thr	Cys	Gln	
				125					130					135	
Ser	Asp	Val	Asp	Glu	Cys	Ser	Ala	Arg	Arg	Gly	Gly	Cys	Pro	Gln	
				140					145					150	
Arg	Cys	Ile	Asn	Thr	Ala	Gly	Ser	Tyr	Trp	Cys	Gln	Cys	Trp	Glu	
				155					160					165	
Gly	His	Ser	Leu	Ser	Ala	Asp	Gly	Thr	Leu	Cys	Val	Pro	Lys	Gly	
				170					175					180	
Gly	Pro	Pro	Arg	Val	Ala	Pro	Asn	Pro	Thr	Gly	Val	Asp	Ser	Ala	
				185					190					195	
Met	Lys	Glu	Glu	Val	Gln	Arg	Leu	Gln	Ser	Arg	Val	Asp	Leu	Leu	
				200					205					210	
Glu	Glu	Lys	Leu	Gln	Leu	Val	Leu	Ala	Pro	Leu	His	Ser	Leu	Ala	
				215					220					225	
Ser	Gln	Ala	Leu	Glu	His	Gly	Leu	Pro	Asp	Pro	Gly	Ser	Leu	Leu	
				230					235					240	
Val	His	Ser	Phe	Gln	Gln	Leu	Gly	Arg	Ile	Asp	Ser	Leu	Ser	Glu	
				245					250					255	
Gln	Ile	Ser	Phe	Leu	Glu	Glu	Gln	Leu	Gly	Ser	Cys	Ser	Cys	Lys	
				260					265					270	

Lys Asp Ser

<210> 509

<211> 1538

<212> DNA

<213> Homo sapiens

<400> 509

cccacgcgtc cgaagctggc cctgcacggc tgcaagggag gctcctgtgg 50

acaggccagg caggtgggcc tcaggaggtg cctccaggcg gccagtgggc 100  
ctgaggcccc agcaagggct aggggtccatc tccagtccca ggacacagca 150  
gcggccacca tggccacgcc tgggctccag cagcatcagc agcccccagg 200  
accggggagg cacaggtggc ccccaccacc cggaggagca gtcctgccc 250  
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tgctaggagg ggcggctgtc cccagcgctg cgtcaacacc gccggcagtt 800  
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tgtgtgccc a agggagggcc ccccagggtg gcccacaacc cgacaggagt 900  
ggacagtgca atgaagggaag aagtgcagag gctgcagtcc aggggtggacc 950  
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ctgctgcctg acccccagca caataaaaat gaaacgtg 1538

<210> 510

<211> 273

<212> PRT

<213> Homo sapiens

<400> 510

Met	Arg	Gly	Ser	Gln	Glu	Val	Leu	Leu	Met	Trp	Leu	Leu	Val	Leu	
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Ala	Val	Gly	Gly	Thr	Glu	His	Ala	Tyr	Arg	Pro	Gly	Arg	Arg	Val	
				20					25					30	
Cys	Ala	Val	Arg	Ala	His	Gly	Asp	Pro	Val	Ser	Glu	Ser	Phe	Val	
				35					40					45	
Gln	Arg	Val	Tyr	Gln	Pro	Phe	Leu	Thr	Thr	Cys	Asp	Gly	His	Arg	
				50					55					60	
Ala	Cys	Ser	Thr	Tyr	Arg	Thr	Ile	Tyr	Arg	Thr	Ala	Tyr	Arg	Arg	
				65					70					75	
Ser	Pro	Gly	Leu	Ala	Pro	Ala	Arg	Pro	Arg	Tyr	Ala	Cys	Cys	Pro	
				80					85					90	
Gly	Trp	Lys	Arg	Thr	Ser	Gly	Leu	Pro	Gly	Ala	Cys	Gly	Ala	Ala	
				95					100					105	
Ile	Cys	Gln	Pro	Pro	Cys	Arg	Asn	Gly	Gly	Ser	Cys	Val	Gln	Pro	
				110					115					120	
Gly	Arg	Cys	Arg	Cys	Pro	Ala	Gly	Trp	Arg	Gly	Asp	Thr	Cys	Gln	
				125					130					135	
Ser	Asp	Val	Asp	Glu	Cys	Ser	Ala	Arg	Arg	Gly	Gly	Cys	Pro	Gln	
				140					145					150	
Arg	Cys	Val	Asn	Thr	Ala	Gly	Ser	Tyr	Trp	Cys	Gln	Cys	Trp	Glu	
				155					160					165	
Gly	His	Ser	Leu	Ser	Ala	Asp	Gly	Thr	Leu	Cys	Val	Pro	Lys	Gly	
				170					175					180	
Gly	Pro	Pro	Arg	Val	Ala	Pro	Asn	Pro	Thr	Gly	Val	Asp	Ser	Ala	
				185					190					195	
Met	Lys	Glu	Glu	Val	Gln	Arg	Leu	Gln	Ser	Arg	Val	Asp	Leu	Leu	
				200					205					210	
Glu	Glu	Lys	Leu	Gln	Leu	Val	Leu	Ala	Pro	Leu	His	Ser	Leu	Ala	
				215					220					225	
Ser	Gln	Ala	Leu	Glu	His	Gly	Leu	Pro	Asp	Pro	Gly	Ser	Leu	Leu	
				230					235					240	



Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu  
245 250 255

Gln Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys  
260 265 270

Lys Asp Ser

<210> 511  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 511  
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<210> 512  
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<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 512  
ttttccactc ctgtcgggtt gg 22

<210> 513  
<211> 46  
<212> DNA  
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<220>  
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<400> 513  
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<210> 514  
<211> 2690  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 2039-2065  
<223> unknown base

<400> 514  
ggttgccaca gctggtttag ggccccgacc actggggccc cttgtcagga 50  
ggagacagcc tccccggccg gggaggacaa gtcgctgcca cctttggctg 100

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agttgggtct ccgtgtttca ggccggctcc cccttcctgg tctcccttct 200  
cccgtctggc cggtttatcg ggaggagatt gtcttccagg gctagcaatt 250  
ggacttttga tgatgtttga ccagcggca ggaatagcag gcaacgtgat 300  
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atggccgcgt catgatggcc cggcaaaagg gcattttcta cctgaccctt 500  
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 gggatcctaa ctgggttctt ggggtcttca ggactgaaga ggaggagag 1950  
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 ccttttagga atgggacagg taccttccac ttgttgtann nnnnnnnnnn 2050  
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 caccggcaga gtcccagagc cacttcaccc tgggggtggg ctgtggcccc 2500  
 cagtcagctc tgctcaggac ctgctctatt tcagggaaga agatttatgt 2550  
 attatatgtg gctatatattc ctagagcacc tgtgttttcc tctttctaag 2600  
 ccagggtcct gtctggatga cttatgcggt gggggagtgt aaaccggaac 2650  
 tttcatcta tttgaaggcg attaaactgt gtctaatagca 2690

<210> 515

<211> 364

<212> PRT

<213> Homo sapiens

<400> 515

Met	Ser	Val	Met	Val	Val	Arg	Lys	Lys	Val	Thr	Arg	Lys	Trp	Glu
1				5					10					15

Lys Leu Pro Gly Arg Asn Thr Phe Cys Cys Asp Gly Arg Val Met

20										25					30				
Met	Ala	Arg	Gln	Lys	Gly	Ile	Phe	Tyr	Leu	Thr	Leu	Phe	Leu	Ile					
				35					40					45					
Leu	Gly	Thr	Cys	Thr	Leu	Phe	Phe	Ala	Phe	Glu	Cys	Arg	Tyr	Leu					
				50					55					60					
Ala	Val	Gln	Leu	Ser	Pro	Ala	Ile	Pro	Val	Phe	Ala	Ala	Met	Leu					
				65					70					75					
Phe	Leu	Phe	Ser	Met	Ala	Thr	Leu	Leu	Arg	Thr	Ser	Phe	Ser	Asp					
				80					85					90					
Pro	Gly	Val	Ile	Pro	Arg	Ala	Leu	Pro	Asp	Glu	Ala	Ala	Phe	Ile					
				95					100					105					
Glu	Met	Glu	Ile	Glu	Ala	Thr	Asn	Gly	Ala	Val	Pro	Gln	Gly	Gln					
				110					115					120					
Arg	Pro	Pro	Pro	Arg	Ile	Lys	Asn	Phe	Gln	Ile	Asn	Asn	Gln	Ile					
				125					130					135					
Val	Lys	Leu	Lys	Tyr	Cys	Tyr	Thr	Cys	Lys	Ile	Phe	Arg	Pro	Pro					
				140					145					150					
Arg	Ala	Ser	His	Cys	Ser	Ile	Cys	Asp	Asn	Cys	Val	Glu	Arg	Phe					
				155					160					165					
Asp	His	His	Cys	Pro	Trp	Val	Gly	Asn	Cys	Val	Gly	Lys	Arg	Asn					
				170					175					180					
Tyr	Arg	Tyr	Phe	Tyr	Leu	Phe	Ile	Leu	Ser	Leu	Ser	Leu	Leu	Thr					
				185					190					195					
Ile	Tyr	Val	Phe	Ala	Phe	Asn	Ile	Val	Tyr	Val	Ala	Leu	Lys	Ser					
				200					205					210					
Leu	Lys	Ile	Gly	Phe	Leu	Glu	Thr	Leu	Lys	Glu	Thr	Pro	Gly	Thr					
				215					220					225					
Val	Leu	Glu	Val	Leu	Ile	Cys	Phe	Phe	Thr	Leu	Trp	Ser	Val	Val					
				230					235					240					
Gly	Leu	Thr	Gly	Phe	His	Thr	Phe	Leu	Val	Ala	Leu	Asn	Gln	Thr					
				245					250					255					
Thr	Asn	Glu	Asp	Ile	Lys	Gly	Ser	Trp	Thr	Gly	Lys	Asn	Arg	Val					
				260					265					270					
Gln	Asn	Pro	Tyr	Ser	His	Gly	Asn	Ile	Val	Lys	Asn	Cys	Cys	Glu					
				275					280					285					
Val	Leu	Cys	Gly	Pro	Leu	Pro	Pro	Ser	Val	Leu	Asp	Arg	Arg	Gly					
				290					295					300					
Ile	Leu	Pro	Leu	Glu	Glu	Ser	Gly	Ser	Arg	Pro	Pro	Ser	Thr	Gln					

	305		310		315
Glu Thr Ser Ser	Ser Leu Leu Pro Gln Ser Pro Ala Pro Thr Glu				
	320		325		330
His Leu Asn Ser	Asn Glu Met Pro Glu Asp Ser Ser Thr Pro Glu				
	335		340		345
Glu Met Pro Pro	Pro Glu Pro Pro Glu Pro Pro Gln Glu Ala Ala				
	350		355		360
Glu Ala Glu Lys					

<210> 516  
 <211> 255  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 36, 38, 88, 118, 135, 193, 213, 222  
 <223> unknown base

<400> 516  
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 tgaattaggt attatagga tgggtggggtt gatttttntt cctggaggct 100  
 tttggctttg gactctcnct ttctcccaca gagencttcg accatcactg 150  
 cccctgggtg gggaattgtg ttggaaagag gaactaccgc tanttctacc 200  
 tcttcactct ttntctctcc cncctcaciaa tctatgtctt cgccttcaac 250  
 atcgt 255

<210> 517  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 517  
 caacgtgatt tcaaagctgg gctc 24

<210> 518  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 518

gcctcgtatc aagaatttcc 20

<210> 519

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 519

agtggaagtc gacctccc 18

<210> 520

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 520

ctcacctgaa atctctcata gcc 24

<210> 521

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 521

cgcaaaaccc attttgggag caggaattcc aatcatgtct gtgatgggtg 50

<210> 522

<211> 1679

<212> DNA

<213> Homo sapiens

<400> 522

gttgtgtcct tcagcaaaac agtggattta aatctccttg cacaagcttg 50

agagcaacac aatctatcag gaaagaaaga aagaaaaaaa ccgaacctga 100

caaaaaagaa gaaaaagaag aagaaaaaaa atcatgaaaa ccatccagcc 150

aaaaatgcac aattctatct cttgggcaat cttcacgggg ctggctgctc 200

tgtgtctctt ccaaggagtg cccgtgcgca gcggagatgc caccttcccc 250

aaagctatgg acaacgtgac ggtccggcag ggggagagcg ccaccctcag 300

gtgcactatt gacaaccggg tcaccgggtt ggcctggcta aaccgcagca 350

ccatcctcta tgctgggaat gacaagtggg gcctggatcc tcgctgggtc 400

cttctgagca acacccaaac gcagtagacg atcgagatcc agaacgtgga 450  
 tgtgtatgac gagggccctt acacctgctc ggtgcagaca gacaaccacc 500  
 caaagacctc taggggccac ctcatgtgac aagtatctcc caaaattgta 550  
 gagatttctt cagatatctc cattaatgaa gggaacaata ttagcctcac 600  
 ctgcatagca actggtagac cagagcctac gggtacttgg agacacatct 650  
 ctoccaaagc gggtggcttt gtgagtgaag acgaatactt ggaaattcag 700  
 ggcatcaccg gggagcagtc aggggactac gagtgcagtg cctccaatga 750  
 cgtggccgcg cccgtggtac ggagagtaaa ggtcaccgtg aactatccac 800  
 catacatttc agaagccaag ggtacaggtg tccccgtggg aaaaagggg 850  
 aactgcagtg gtgaagcctc agcagtcctc tcagcagaat tccagtggta 900  
 caaggatgac aaaagactga ttgaaggaaa gaaaggggtg aaagtggaaa 950  
 acagaccttt cctctcaaaa ctcatcttct tcaatgtctc tgaacatgac 1000  
 tatgggaact acacttgctg ggctccaac aagctgggac acaccaatgc 1050  
 cagcatcatg ctatttggtc caggcgccgt cagcgaggtg agcaacggca 1100  
 cgtcgaggag ggcaggctgc gtctggctgc tgctcttctt ggtcttgac 1150  
 ctgcttctca aattttgatg tgagtgccac ttccccaccg gggaaaggct 1200  
 gccgccacca ccaccaccaa cacaacagca atggcaacac cgacagcaac 1250  
 caatcagata tatacaaatg aaattagaag aaacacagcc tcatgggaca 1300  
 gaaatttgag ggaggggaac aaagaatact ttggggggaa aagagtttta 1350  
 aaaaagaaat tgaaaattgc cttgcagata tttaggtaca atggagtttt 1400  
 cttttcccaa acgggaagaa cacagcacac ccggcttgga cccactgcaa 1450  
 gctgcatcgt gcaacctctt tggtgccagt gtgggcaagg gctcagcctc 1500  
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 aattcaatca gtccatagag acgaacagaa tgagaccttc cggcccaagc 1600  
 gtggcgctgc gggcactttg gtagactgtg ccaccacggc gtgtgtgtgtg 1650  
 aaacgtgaaa taaaagagc aaaaaaaaaa 1679

<210> 523  
 <211> 344  
 <212> PRT  
 <213> Homo sapiens

<400> 523

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Ile	Phe	Thr	Gly	Leu	Ala	Ala	Leu	Cys	Leu	Phe	Gln	Gly	Val	Pro	
				20					25					30	
Val	Arg	Ser	Gly	Asp	Ala	Thr	Phe	Pro	Lys	Ala	Met	Asp	Asn	Val	
				35					40					45	
Thr	Val	Arg	Gln	Gly	Glu	Ser	Ala	Thr	Leu	Arg	Cys	Thr	Ile	Asp	
				50					55					60	
Asn	Arg	Val	Thr	Arg	Val	Ala	Trp	Leu	Asn	Arg	Ser	Thr	Ile	Leu	
				65					70					75	
Tyr	Ala	Gly	Asn	Asp	Lys	Trp	Cys	Leu	Asp	Pro	Arg	Val	Val	Leu	
				80					85					90	
Leu	Ser	Asn	Thr	Gln	Thr	Gln	Tyr	Ser	Ile	Glu	Ile	Gln	Asn	Val	
				95					100					105	
Asp	Val	Tyr	Asp	Glu	Gly	Pro	Tyr	Thr	Cys	Ser	Val	Gln	Thr	Asp	
				110					115					120	
Asn	His	Pro	Lys	Thr	Ser	Arg	Val	His	Leu	Ile	Val	Gln	Val	Ser	
				125					130					135	
Pro	Lys	Ile	Val	Glu	Ile	Ser	Ser	Asp	Ile	Ser	Ile	Asn	Glu	Gly	
				140					145					150	
Asn	Asn	Ile	Ser	Leu	Thr	Cys	Ile	Ala	Thr	Gly	Arg	Pro	Glu	Pro	
				155					160					165	
Thr	Val	Thr	Trp	Arg	His	Ile	Ser	Pro	Lys	Ala	Val	Gly	Phe	Val	
				170					175					180	
Ser	Glu	Asp	Glu	Tyr	Leu	Glu	Ile	Gln	Gly	Ile	Thr	Arg	Glu	Gln	
				185					190					195	
Ser	Gly	Asp	Tyr	Glu	Cys	Ser	Ala	Ser	Asn	Asp	Val	Ala	Ala	Pro	
				200					205					210	
Val	Val	Arg	Arg	Val	Lys	Val	Thr	Val	Asn	Tyr	Pro	Pro	Tyr	Ile	
				215					220					225	
Ser	Glu	Ala	Lys	Gly	Thr	Gly	Val	Pro	Val	Gly	Gln	Lys	Gly	Thr	
				230					235					240	
Leu	Gln	Cys	Glu	Ala	Ser	Ala	Val	Pro	Ser	Ala	Glu	Phe	Gln	Trp	
				245					250					255	
Tyr	Lys	Asp	Asp	Lys	Arg	Leu	Ile	Glu	Gly	Lys	Lys	Gly	Val	Lys	
				260					265					270	
Val	Glu	Asn	Arg	Pro	Phe	Leu	Ser	Lys	Leu	Ile	Phe	Phe	Asn	Val	
				275					280					285	



Ser Glu His Asp Tyr Gly Asn Tyr Thr Cys Val Ala Ser Asn Lys  
290 295 300

Leu Gly His Thr Asn Ala Ser Ile Met Leu Phe Gly Pro Gly Ala  
305 310 315

Val Ser Glu Val Ser Asn Gly Thr Ser Arg Arg Ala Gly Cys Val  
320 325 330

Trp Leu Leu Pro Leu Leu Val Leu His Leu Leu Leu Lys Phe  
335 340

<210> 524  
<211> 503  
<212> DNA  
<213> Homo sapiens

<400> 524  
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cgtgcgcagc ggagatgcca ccttcccaa agctatggac aacgtgacgg 150  
tccggcaggg ggagagcgcc accctcaggt gcactattga caaccgggtc 200  
acccgggtgg cctggctaaa ccgcagcacc atcctctatg ctgggaatga 250  
caagtgggtgc ctggatcctc gcgtggtcct tctgagcaac acccaaacgc 300  
agtacagcat cgagatccag aacgtggatg tgtatgacga gggcccttac 350  
acctgctcgg tgcagacaga caaccacca aagacctcta gggtcacact 400  
cattgtgcaa gtatctccca aaattgtaga gatttcttca gatatctcca 450  
ttaatgaagg gaacaatatt agcctcacct gcatagcaac tggtagacca 500  
gag 503

<210> 525  
<211> 2602  
<212> DNA  
<213> Homo sapiens

<400> 525  
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gcggggccagc tgccgggagc cctgaatcac cgctggccc gactccacca 100  
tgaacgtcgc gctgcaggag ctgggagctg gcagcaacgt gggattccag 150  
aaggggacaa gacagctgtt aggctcacgc acgcagctgg agctggtctt 200  
agcaggtgcc tctctactgc tggctgcact gcttctgggc tgccttgtgg 250

ccctaggggt ccagtaccac agagacccat cccacagcac ctgccttaca 300  
gaggcctgca ttcgagtggc tggaaaaatc ctggagtccc tggaccgagg 350  
ggtgagcccc tgtgaggact tttaccagtt ctctgtggg ggctggattc 400  
ggaggaaccc cctgcccgat gggcggttctc gctggaacac cttcaacagc 450  
ctctgggacc aaaaccaggc catactgaag cacctgcttg aaaacaccac 500  
cttcaactcc agcagtgaag ctgagcagaa gacacagcgc ttctacctat 550  
cttgccctaca ggtggagcgc attgaggagc tgggagccca gccactgaga 600  
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ccccattctt caccgtctac atcagtgccg actctaagag ttccaacagc 750  
aatgttatcc aggtggacca gtctgggctc tttctgccct ctcgggatta 800  
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gagcagatgc agcagggtgt ggagttggag atacagctgg ccaacatcac 950  
agtgccccag gaccagcggc gcgacgagga gaagatctac cacaagatga 1000  
gcatttcgga gctgcaggct ctggcgccct ccatggactg gcttgagttc 1050  
ctgtctttct tgctgtcacc attggagttg agtgactctg agcctgtggt 1100  
ggtgtatggg atggattatt tgcagcagggt gtcagagctc atcaaccgca 1150  
cggaaccaag catcctgaac aattacctga tctggaacct ggtgcaaaag 1200  
acaacctcaa gcctggaccg acgctttgag tctgcacaag agaagctgct 1250  
ggagaccctc tatggcacta agaagtcctg tgtgccgagg tggcagacct 1300  
gcatctccaa cacggatgac gcccttggtt ttgctttggg gtcactcttc 1350  
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cagcgaaatc cggaccgcat ttgaggaggc cctgggacag ctggtttgga 1450  
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ggtgtggtca tgggccatga gttgacgcat gcctttgatg accaagggcg 1850  
cgagtatgac aaagaaggga acctgcgggc ctgggtggcag aatgagtccc 1900  
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cagaccctcc tcaatcacca cattgtgcct ctgctttggg ggtgcccctg 2500  
cctccagcag agccccacc attcactgtg acatctttcc gtgtcacct 2550  
gcctggaaga ggtctgggtg gggaggccag ttcccatagg aaggagtctg 2600  
cc 2602

<210> 526

<211> 736

<212> PRT

<213> Homo sapiens

<400> 526

Met	Asn	Val	Ala	Leu	Gln	Glu	Leu	Gly	Ala	Gly	Ser	Asn	Val	Gly
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Phe	Gln	Lys	Gly	Thr	Arg	Gln	Leu	Leu	Gly	Ser	Arg	Thr	Gln	Leu
				20					25					30
Glu	Leu	Val	Leu	Ala	Gly	Ala	Ser	Leu	Leu	Leu	Ala	Ala	Leu	Leu
				35					40					45
Leu	Gly	Cys	Leu	Val	Ala	Leu	Gly	Val	Gln	Tyr	His	Arg	Asp	Pro
				50					55					60

Ser	His	Ser	Thr	Cys	Leu	Thr	Glu	Ala	Cys	Ile	Arg	Val	Ala	Gly		65	70	75
Lys	Ile	Leu	Glu	Ser	Leu	Asp	Arg	Gly	Val	Ser	Pro	Cys	Glu	Asp		80	85	90
Phe	Tyr	Gln	Phe	Ser	Cys	Gly	Gly	Trp	Ile	Arg	Arg	Asn	Pro	Leu		95	100	105
Pro	Asp	Gly	Arg	Ser	Arg	Trp	Asn	Thr	Phe	Asn	Ser	Leu	Trp	Asp		110	115	120
Gln	Asn	Gln	Ala	Ile	Leu	Lys	His	Leu	Leu	Glu	Asn	Thr	Thr	Phe		125	130	135
Asn	Ser	Ser	Ser	Glu	Ala	Glu	Gln	Lys	Thr	Gln	Arg	Phe	Tyr	Leu		140	145	150
Ser	Cys	Leu	Gln	Val	Glu	Arg	Ile	Glu	Glu	Leu	Gly	Ala	Gln	Pro		155	160	165
Leu	Arg	Asp	Leu	Ile	Glu	Lys	Ile	Gly	Gly	Trp	Asn	Ile	Thr	Gly		170	175	180
Pro	Trp	Asp	Gln	Asp	Asn	Phe	Met	Glu	Val	Leu	Lys	Ala	Val	Ala		185	190	195
Gly	Thr	Tyr	Arg	Ala	Thr	Pro	Phe	Phe	Thr	Val	Tyr	Ile	Ser	Ala		200	205	210
Asp	Ser	Lys	Ser	Ser	Asn	Ser	Asn	Val	Ile	Gln	Val	Asp	Gln	Ser		215	220	225
Gly	Leu	Phe	Leu	Pro	Ser	Arg	Asp	Tyr	Tyr	Leu	Asn	Arg	Thr	Ala		230	235	240
Asn	Glu	Lys	Val	Leu	Thr	Ala	Tyr	Leu	Asp	Tyr	Met	Glu	Glu	Leu		245	250	255
Gly	Met	Leu	Leu	Gly	Gly	Arg	Pro	Thr	Ser	Thr	Arg	Glu	Gln	Met		260	265	270
Gln	Gln	Val	Leu	Glu	Leu	Glu	Ile	Gln	Leu	Ala	Asn	Ile	Thr	Val		275	280	285
Pro	Gln	Asp	Gln	Arg	Arg	Asp	Glu	Glu	Lys	Ile	Tyr	His	Lys	Met		290	295	300
Ser	Ile	Ser	Glu	Leu	Gln	Ala	Leu	Ala	Pro	Ser	Met	Asp	Trp	Leu		305	310	315
Glu	Phe	Leu	Ser	Phe	Leu	Leu	Ser	Pro	Leu	Glu	Leu	Ser	Asp	Ser		320	325	330
Glu	Pro	Val	Val	Val	Tyr	Gly	Met	Asp	Tyr	Leu	Gln	Gln	Val	Ser		335	340	345

Glu	Leu	Ile	Asn	Arg	Thr	Glu	Pro	Ser	Ile	Leu	Asn	Asn	Tyr	Leu	350	355	360
Ile	Trp	Asn	Leu	Val	Gln	Lys	Thr	Thr	Ser	Ser	Leu	Asp	Arg	Arg	365	370	375
Phe	Glu	Ser	Ala	Gln	Glu	Lys	Leu	Leu	Glu	Thr	Leu	Tyr	Gly	Thr	380	385	390
Lys	Lys	Ser	Cys	Val	Pro	Arg	Trp	Gln	Thr	Cys	Ile	Ser	Asn	Thr	395	400	405
Asp	Asp	Ala	Leu	Gly	Phe	Ala	Leu	Gly	Ser	Leu	Phe	Val	Lys	Ala	410	415	420
Thr	Phe	Asp	Arg	Gln	Ser	Lys	Glu	Ile	Ala	Glu	Gly	Met	Ile	Ser	425	430	435
Glu	Ile	Arg	Thr	Ala	Phe	Glu	Glu	Ala	Leu	Gly	Gln	Leu	Val	Trp	440	445	450
Met	Asp	Glu	Lys	Thr	Arg	Gln	Ala	Ala	Lys	Glu	Lys	Ala	Asp	Ala	455	460	465
Ile	Tyr	Asp	Met	Ile	Gly	Phe	Pro	Asp	Phe	Ile	Leu	Glu	Pro	Lys	470	475	480
Glu	Leu	Asp	Asp	Val	Tyr	Asp	Gly	Tyr	Glu	Ile	Ser	Glu	Asp	Ser	485	490	495
Phe	Phe	Gln	Asn	Met	Leu	Asn	Leu	Tyr	Asn	Phe	Ser	Ala	Lys	Val	500	505	510
Met	Ala	Asp	Gln	Leu	Arg	Lys	Pro	Pro	Ser	Arg	Asp	Gln	Trp	Ser	515	520	525
Met	Thr	Pro	Gln	Thr	Val	Asn	Ala	Tyr	Tyr	Leu	Pro	Thr	Lys	Asn	530	535	540
Glu	Ile	Val	Phe	Pro	Ala	Gly	Ile	Leu	Gln	Ala	Pro	Phe	Tyr	Ala	545	550	555
Arg	Asn	His	Pro	Lys	Ala	Leu	Asn	Phe	Gly	Gly	Ile	Gly	Val	Val	560	565	570
Met	Gly	His	Glu	Leu	Thr	His	Ala	Phe	Asp	Asp	Gln	Gly	Arg	Glu	575	580	585
Tyr	Asp	Lys	Glu	Gly	Asn	Leu	Arg	Pro	Trp	Trp	Gln	Asn	Glu	Ser	590	595	600
Leu	Ala	Ala	Phe	Arg	Asn	His	Thr	Ala	Cys	Met	Glu	Glu	Gln	Tyr	605	610	615
Asn	Gln	Tyr	Gln	Val	Asn	Gly	Glu	Arg	Leu	Asn	Gly	Arg	Gln	Thr	620	625	630

Leu	Gly	Glu	Asn	Ile	Thr	Asp	Asn	Gly	Gly	Leu	Lys	Ala	Ala	Tyr
				635					640					645
Asn	Ala	Tyr	Lys	Ala	Trp	Leu	Arg	Lys	His	Gly	Glu	Glu	Gln	Gln
				650					655					660
Leu	Pro	Ala	Val	Gly	Leu	Thr	Asn	His	Gln	Leu	Phe	Phe	Val	Gly
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Glu	Gly	Leu	Val	Thr	Asp	Pro	His	Ser	Pro	Ala	Arg	Phe	Arg	Val
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gaaagtaacc acggaggtca agat 24

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<223> Synthetic oligonucleotide probe

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<210> 565

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<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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gagagagga aggcagctat gtc 23

<210> 566

<211> 21

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<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<210> 581

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<210> 584  
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<210> 589  
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<210> 590  
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<210> 591  
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<210> 592  
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<400> 592  
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<210> 593  
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<400> 593  
ctttgaatag aagacttctg gacaattt 28

<210> 594  
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<400> 594  
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<210> 595  
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<400> 595  
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<210> 599  
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<210> 606  
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<210> 611  
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acccacccac caaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaatc 200  
ctgtggcgcg ccgcctggtt cccgggaaga ctgccagca ccaggggggtg 250  
ggggagtgcg agctgaaagc tgctggagag tgagcagccc tagcagggat 300  
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<210> 612

<211> 352

<212> PRT

<213> Homo Sapien

<400> 612

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				20					25					30
Pro	Ala	Gly	Gln	Ser	Val	Asp	Phe	Pro	Trp	Ala	Ala	Val	Asp	Asn
				35					40					45
Met	Met	Val	Arg	Lys	Gly	Asp	Thr	Ala	Val	Leu	Arg	Cys	Tyr	Leu
				50					55					60
Glu	Asp	Gly	Ala	Ser	Lys	Gly	Ala	Trp	Leu	Asn	Arg	Ser	Ser	Ile
				65					70					75
Ile	Phe	Ala	Gly	Gly	Asp	Lys	Trp	Ser	Val	Asp	Pro	Arg	Val	Ser
				80					85					90
Ile	Ser	Thr	Leu	Asn	Lys	Arg	Asp	Tyr	Ser	Leu	Gln	Ile	Gln	Asn
				95					100					105
Val	Asp	Val	Thr	Asp	Asp	Gly	Pro	Tyr	Thr	Cys	Ser	Val	Gln	Thr

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Gln	His	Thr	Pro	Arg	Thr	Met	Gln	Val	His	Leu	Thr	Val	Gln	Val
				125										135
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Pro	Ser	Ile	Ser	Trp	Arg	His	Ile	Ser	Pro	Ser	Ala	Lys	Pro	Phe
				170										180
Glu	Asn	Gly	Gln	Tyr	Leu	Asp	Ile	Tyr	Gly	Ile	Thr	Arg	Asp	Gln
				185										195
Ala	Gly	Glu	Tyr	Glu	Cys	Ser	Ala	Glu	Asn	Ala	Val	Ser	Phe	Pro
				200										210
Asp	Val	Arg	Lys	Val	Lys	Val	Val	Val	Asn	Phe	Ala	Pro	Thr	Ile
				215										225
Gln	Glu	Ile	Lys	Ser	Gly	Thr	Val	Thr	Pro	Gly	Arg	Ser	Gly	Leu
				230										240
Ile	Arg	Cys	Glu	Gly	Ala	Gly	Val	Pro	Pro	Pro	Ala	Phe	Glu	Trp
				245										255
Tyr	Lys	Gly	Glu	Lys	Lys	Leu	Phe	Asn	Gly	Gln	Gln	Gly	Ile	Ile
				260										270
Ile	Gln	Asn	Phe	Ser	Thr	Arg	Ser	Ile	Leu	Thr	Val	Thr	Asn	Val
				275										285
Thr	Gln	Glu	His	Phe	Gly	Asn	Tyr	Thr	Cys	Val	Ala	Ala	Asn	Lys
				290										300
Leu	Gly	Thr	Thr	Asn	Ala	Ser	Leu	Pro	Leu	Asn	Pro	Pro	Ser	Thr
				305										315
Ala	Gln	Tyr	Gly	Ile	Thr	Gly	Ser	Ala	Asp	Val	Leu	Phe	Ser	Cys
				320										330
Trp	Tyr	Leu	Val	Leu	Thr	Leu	Ser	Ser	Phe	Thr	Ser	Ile	Phe	Tyr
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Leu	Lys	Asn	Ala	Ile	Leu	Gln								
				350										

<210> 613  
 <211> 1797  
 <212> DNA  
 <213> Homo Sapien

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ctgcttttca ccaaattgca atggagcctt tcgaaatcaa tgttccaaag 200  
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<210> 614

<211> 520

<212> PRT

<213> Homo Sapien

<400> 614

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Ile	Asn	Val	Pro	Lys	Pro	Lys	Arg	Arg	Asn	Gly	Val	Asn	Phe	Ser	35	40	45	
Leu	Ala	Val	Val	Val	Ile	Tyr	Leu	Ile	Leu	Leu	Thr	Ala	Gly	Ala	50	55	60	
Gly	Leu	Leu	Val	Val	Gln	Val	Leu	Asn	Leu	Gln	Ala	Arg	Leu	Arg	65	70	75	
Val	Leu	Glu	Met	Tyr	Phe	Leu	Asn	Asp	Thr	Leu	Ala	Ala	Glu	Asp	80	85	90	
Ser	Pro	Ser	Phe	Ser	Leu	Leu	Gln	Ser	Ala	His	Pro	Gly	Glu	His	95	100	105	
Leu	Ala	Gln	Gly	Ala	Ser	Arg	Leu	Gln	Val	Leu	Gln	Ala	Gln	Leu	110	115	120	
Thr	Trp	Val	Arg	Val	Ser	His	Glu	His	Leu	Leu	Gln	Arg	Val	Asp	125	130	135	
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Gly	Ala	Pro	Gly	Leu	Gln	Gly	His	Lys	Gly	Ala	Met	Gly	Met	Pro	155	160	165	
Gly	Ala	Pro	Gly	Pro	Pro	Gly	Pro	Pro	Ala	Glu	Lys	Gly	Ala	Lys	170	175	180	
Gly	Ala	Met	Gly	Arg	Asp	Gly	Ala	Thr	Gly	Pro	Ser	Gly	Pro	Gln				



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Gly	Ala	Pro	Gly	Lys	Gln	Gly	Ala	Thr	Gly	Thr	Pro	Gly	Pro	Gln
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Gly	Glu	Lys	Gly	Ser	Lys	Gly	Asp	Gly	Gly	Leu	Ile	Gly	Pro	Lys
				230					235					240
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				305					310					315
Gly	His	Pro	Gly	Ala	Lys	Gly	Glu	Pro	Gly	Ser	Ala	Gly	Ser	Pro
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Gly	Arg	Ala	Gly	Leu	Pro	Gly	Ser	Pro	Gly	Ser	Pro	Gly	Ala	Thr
				335					340					345
Gly	Leu	Lys	Gly	Ser	Lys	Gly	Asp	Thr	Gly	Leu	Gln	Gly	Gln	Gln
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Gly	Arg	Lys	Gly	Glu	Ser	Gly	Val	Pro	Gly	Pro	Ala	Gly	Val	Lys
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Gly	Glu	Gln	Gly	Ser	Pro	Gly	Leu	Ala	Gly	Pro	Lys	Gly	Ala	Pro
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Gly	Gln	Ala	Gly	Gln	Lys	Gly	Asp	Gln	Gly	Val	Lys	Gly	Ser	Ser
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Gly	Glu	Gln	Gly	Val	Lys	Gly	Glu	Lys	Gly	Glu	Arg	Gly	Glu	Asn
				410					415					420
Ser	Val	Ser	Val	Arg	Ile	Val	Gly	Ser	Ser	Asn	Arg	Gly	Arg	Ala
				425					430					435
Glu	Val	Tyr	Tyr	Ser	Gly	Thr	Trp	Gly	Thr	Ile	Cys	Asp	Asp	Glu
				440					445					450
Trp	Gln	Asn	Ser	Asp	Ala	Ile	Val	Phe	Cys	Arg	Met	Leu	Gly	Tyr
				455					460					465
Ser	Lys	Gly	Arg	Ala	Leu	Tyr	Lys	Val	Gly	Ala	Gly	Thr	Gly	Gln

	470		475		480
Ile Trp Leu Asp Asn Val Gln Cys Arg Gly Thr Glu Ser Thr Leu					
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Trp Ser Cys Thr Lys Asn Ser Trp Gly His His Asp Cys Ser His					
	500		505		510
Glu Glu Asp Ala Gly Val Glu Cys Ser Val					
	515		520		

<210> 615  
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 <212> DNA  
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 aaaagccaaa atgaaactga tgggtacttgt tttcaccatt gggctaactt 200  
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 aagatactaa aagatcacia ctgtcacaac cttccggaag gagtagctga 300  
 cctgacacag attgatgtca atgtccagga tcatttctgg gatgggaagg 350  
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 tcaatgagaa tcttcatgta ttctggagaa caccattcct gatttccac 500  
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 gttaaacaag tagtaataaa agttaattca atctaaaaaa aaaaaa 647

<210> 616  
 <211> 98  
 <212> PRT  
 <213> Homo Sapien

<400> 616  
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 20 25 30  
 Lys Ile Leu Lys Asp His Asn Cys His Asn Leu Pro Glu Gly Val  
 35 40 45

Ala	Asp	Leu	Thr	Gln	Ile	Asp	Val	Asn	Val	Gln	Asp	His	Phe	Trp
				50					55					60
Asp	Gly	Lys	Gly	Cys	Glu	Met	Ile	Cys	Tyr	Cys	Asn	Phe	Ser	Glu
				65					70					75
Leu	Leu	Cys	Cys	Pro	Lys	Asp	Val	Phe	Phe	Gly	Pro	Lys	Ile	Ser
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Phe	Val	Ile	Pro	Cys	Asn	Asn	Gln							
				95										

<210> 617  
 <211> 2558  
 <212> DNA  
 <213> Homo Sapien

<400> 617  
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 gggccccggg aggcgcgctc tgctcgcgcc gagatgtgga atctccttca 200  
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<210> 618

<211> 750

<212> PRT

<213> Homo Sapien

<400> 618

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Arg	Arg	Pro	Arg	Trp	Leu	Cys	Ala	Gly	Ala	Leu	Val	Leu	Ala	Gly
				20					25					30

Gly	Phe	Phe	Leu	Leu	Gly	Phe	Leu	Phe	Gly	Trp	Phe	Ile	Lys	Ser
			35						40					45

Ser	Asn	Glu	Ala	Thr	Asn	Ile	Thr	Pro	Lys	His	Asn	Met	Lys	Ala
			50						55					60

Phe	Leu	Asp	Glu	Leu	Lys	Ala	Glu	Asn	Ile	Lys	Lys	Phe	Leu	His
			65						70					75

Asn	Phe	Thr	Gln	Ile	Pro	His	Leu	Ala	Gly	Thr	Glu	Gln	Asn	Phe
			80						85					90

Gln	Leu	Ala	Lys	Gln	Ile	Gln	Ser	Gln	Trp	Lys	Glu	Phe	Gly	Leu
			95						100					105

Asp	Ser	Val	Glu	Leu	Ala	His	Tyr	Asp	Val	Leu	Leu	Ser	Tyr	Pro
			110						115					120

Asn	Lys	Thr	His	Pro	Asn	Tyr	Ile	Ser	Ile	Ile	Asn	Glu	Asp	Gly
			125						130					135

Asn	Glu	Ile	Phe	Asn	Thr	Ser	Leu	Phe	Glu	Pro	Pro	Pro	Pro	Gly
			140						145					150

Tyr	Glu	Asn	Val	Ser	Asp	Ile	Val	Pro	Pro	Phe	Ser	Ala	Phe	Ser
			155						160					165

Pro	Gln	Gly	Met	Pro	Glu	Gly	Asp	Leu	Val	Tyr	Val	Asn	Tyr	Ala
			170						175					180

Arg	Thr	Glu	Asp	Phe	Phe	Lys	Leu	Glu	Arg	Asp	Met	Lys	Ile	Asn
			185						190					195

Cys	Ser	Gly	Lys	Ile	Val	Ile	Ala	Arg	Tyr	Gly	Lys	Val	Phe	Arg
			200						205					210

Gly Asn Lys Val	Lys Asn Ala Gln Leu	Ala Gly Ala Lys Gly	Val
215	220	225	
Ile Leu Tyr Ser	Asp Pro Ala Asp Tyr	Phe Ala Pro Gly Val	Lys
230	235	240	
Ser Tyr Pro Asp	Gly Trp Asn Leu Pro	Gly Gly Gly Val Gln	Arg
245	250	255	
Gly Asn Ile Leu	Asn Leu Asn Gly Ala	Gly Asp Pro Leu Thr	Pro
260	265	270	
Gly Tyr Pro Ala	Asn Glu Tyr Ala Tyr	Arg Arg Gly Ile Ala	Glu
275	280	285	
Ala Val Gly Leu	Pro Ser Ile Pro Val	His Pro Ile Gly Tyr	Tyr
290	295	300	
Asp Ala Gln Lys	Leu Leu Glu Lys Met	Gly Gly Ser Ala Pro	Pro
305	310	315	
Asp Ser Ser Trp	Arg Gly Ser Leu Lys	Val Pro Tyr Asn Val	Gly
320	325	330	
Pro Gly Phe Thr	Gly Asn Phe Ser Thr	Gln Lys Val Lys Met	His
335	340	345	
Ile His Ser Thr	Asn Glu Val Thr Arg	Ile Tyr Asn Val Ile	Gly
350	355	360	
Thr Leu Arg Gly	Ala Val Glu Pro Asp	Arg Tyr Val Ile Leu	Gly
365	370	375	
Gly His Arg Asp	Ser Trp Val Phe Gly	Gly Ile Asp Pro Gln	Ser
380	385	390	
Gly Ala Ala Val	Val His Glu Ile Val	Arg Ser Phe Gly Thr	Leu
395	400	405	
Lys Lys Glu Gly	Trp Arg Pro Arg Arg	Thr Ile Leu Phe Ala	Ser
410	415	420	
Trp Asp Ala Glu	Glu Phe Gly Leu Leu	Gly Ser Thr Glu Trp	Ala
425	430	435	
Glu Glu Asn Ser	Arg Leu Leu Gln Glu	Arg Gly Val Ala Tyr	Ile
440	445	450	
Asn Ala Asp Ser	Ser Ile Glu Gly Asn	Tyr Thr Leu Arg Val	Asp
455	460	465	
Cys Thr Pro Leu	Met Tyr Ser Leu Val	His Asn Leu Thr Lys	Glu
470	475	480	
Leu Lys Ser Pro	Asp Glu Gly Phe Glu	Gly Lys Ser Leu Tyr	Glu
485	490	495	

Ser	Trp	Thr	Lys	Lys	Ser	Pro	Ser	Pro	Glu	Phe	Ser	Gly	Met	Pro	500	505	510
Arg	Ile	Ser	Lys	Leu	Gly	Ser	Gly	Asn	Asp	Phe	Glu	Val	Phe	Phe	515	520	525
Gln	Arg	Leu	Gly	Ile	Ala	Ser	Gly	Arg	Ala	Arg	Tyr	Thr	Lys	Asn	530	535	540
Trp	Glu	Thr	Asn	Lys	Phe	Ser	Gly	Tyr	Pro	Leu	Tyr	His	Ser	Val	545	550	555
Tyr	Glu	Thr	Tyr	Glu	Leu	Val	Glu	Lys	Phe	Tyr	Asp	Pro	Met	Phe	560	565	570
Lys	Tyr	His	Leu	Thr	Val	Ala	Gln	Val	Arg	Gly	Gly	Met	Val	Phe	575	580	585
Glu	Leu	Ala	Asn	Ser	Ile	Val	Leu	Pro	Phe	Asp	Cys	Arg	Asp	Tyr	590	595	600
Ala	Val	Val	Leu	Arg	Lys	Tyr	Ala	Asp	Lys	Ile	Tyr	Ser	Ile	Ser	605	610	615
Met	Lys	His	Pro	Gln	Glu	Met	Lys	Thr	Tyr	Ser	Val	Ser	Phe	Asp	620	625	630
Ser	Leu	Phe	Ser	Ala	Val	Lys	Asn	Phe	Thr	Glu	Ile	Ala	Ser	Lys	635	640	645
Phe	Ser	Glu	Arg	Leu	Gln	Asp	Phe	Asp	Lys	Ser	Asn	Pro	Ile	Val	650	655	660
Leu	Arg	Met	Met	Asn	Asp	Gln	Leu	Met	Phe	Leu	Glu	Arg	Ala	Phe	665	670	675
Ile	Asp	Pro	Leu	Gly	Leu	Pro	Asp	Arg	Pro	Phe	Tyr	Arg	His	Val	680	685	690
Ile	Tyr	Ala	Pro	Ser	Ser	His	Asn	Lys	Tyr	Ala	Gly	Glu	Ser	Phe	695	700	705
Pro	Gly	Ile	Tyr	Asp	Ala	Leu	Phe	Asp	Ile	Glu	Ser	Lys	Val	Asp	710	715	720
Pro	Ser	Lys	Ala	Trp	Gly	Glu	Val	Lys	Arg	Gln	Ile	Tyr	Val	Ala	725	730	735
Ala	Phe	Thr	Val	Gln	Ala	Ala	Ala	Glu	Thr	Leu	Ser	Glu	Val	Ala	740	745	750

<210> 619

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 619

agatgtgaag gtgcaggtgt gccg 24

<210> 620

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 620

gaacatcagc gctcccggta attcc 25

<210> 621

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 621

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<210> 622

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 622

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<210> 623

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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 623

tgggaaatca ggaatggtgt tctcc 25

<210> 624

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide probe



<400> 624

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